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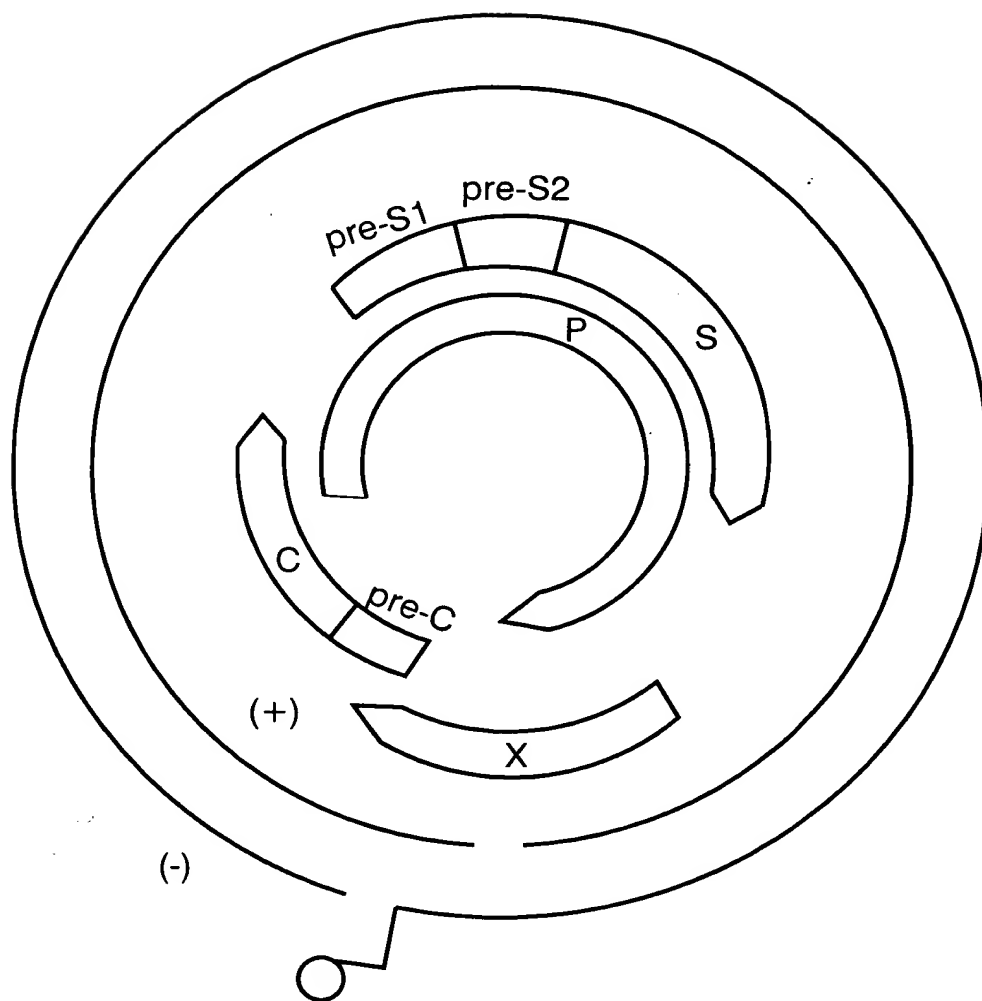


Figure 1A

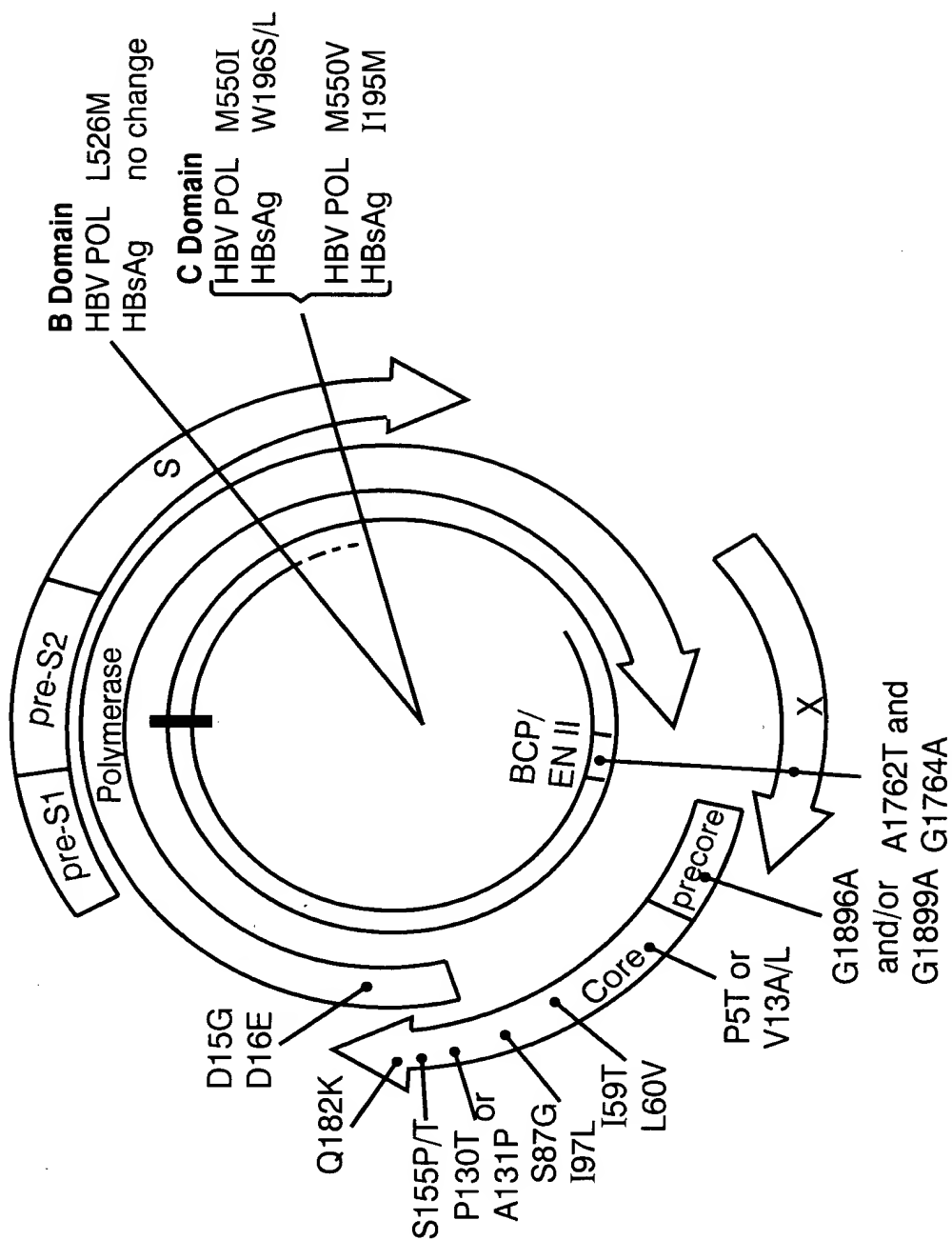


Figure 1B



(421) 430 440 450
 422 438
SNDLSWLSLD VSAAFYHI_PPL HPAAMPHELLIV GSSGL_DRYVA

Domain A

HBsAg G112R T123P Y/F134S D144E G145R
 460 470 480 490
 464 466 477 488 499
 RLSS_T_NSR_NNI*_N NY_HQY_HG_R***_DNLH _DN_YSCSR_DQLYVS LL_MLLYK_QTY_FG_R_W

HBsAg A157D E164D F170L
 500 510 520 530
 512 519 523/524/526/528/530
 KLHL_Y_LSAHPII_V LGFRK_I_LPMG_V_G GLSPFLLAQF TSAIC_L_{SA}_V_M_V_T_R_C_R

Domain B

HBsAg W196L W199S
M195I/S196W M198I S204T S210R
 540 550 560
 546 550 553 559 565
 AFF_PHCL_V_{AV}FS_{AY} MDDV_LMVLGAK_RS_T V_GQ_EHL_{SR}ES_FLY_F_T_{AS}_A

Domain C

570 580 590
 575
 I_V_T_C_NS_F_VLL_S_D_L_VGI HLNP_N_QKTKRW GYSLNFMGYI_V_I G

Domain D

Domain E

Figure 2

[illegible]

A-----A

Figure 3A



042904

A-----A

P₁₀₈ L L₁₁₀ P R

*329616/HPBADR1CG
221499/HPBADW3
221500/HPBCG
62280/XXHEPAV
59439/HBVAYWE
59429/HBVAYWC
59418/HBVADW2
59408/HBVADRM
59404/HBVADR4
329640/HPBAYW
313780/HBVAYWMCG
229417/HPBADW1

5/47

ACTA	C	CAAGGT	ATGT	GT	CT	GT	TT	GT	CC	CT	CT	A	C	TT	CC	A	G		
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	C	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	C	TT	CC	A	G
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	C	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	C	TT	CC	A	G
ACTA	C	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	C	TT	CC	A	G
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	
ACTA	T	CAAGGT	ATGT	TT	GT	CC	CG	TT	TT	GT	CC	CT	CT	A	TT	CC	A	G	

B-----B

Figure 3B



042904

B - - - - -

T	S	T	T	S	T	G	P ₁₂₀	C	K	T	C	T
---	---	---	---	---	---	---	------------------	---	---	---	---	---

*329616/HPBADRI/CG

221499/HPBADW3

221500/HPBCG

62280/XXHEPAV

59439/HBVAYWE

59429/HBVAYWC

59418/HBVADW2

59408/HBVADRM

59404/HBVADR4

329640/HPBAYW

313780/HBVAYWMCG

229417/HPBADW1

A	A	C	A	T	C	A	A	C	T	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G
A	T	C	A	T	C	A	A	C	C	A	C	C	A	G	C	A	T	G	C	A	A	A	A	C	C	T	G	C	A	C	G
A	A	C	A	T	C	A	A	C	T	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G
A	T	C	T	T	C	A	A	C	T	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G
A	T	C	T	T	C	A	A	C	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G	
A	T	C	T	T	C	A	A	C	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G	
A	T	C	A	A	C	A	A	C	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G	
A	A	C	A	T	C	A	A	C	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G	
A	A	C	A	T	C	A	A	C	T	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G
A	T	C	T	T	C	A	A	C	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G	
A	T	C	T	T	C	A	A	C	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G	
A	T	C	A	T	C	A	A	C	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G	
A	T	C	A	T	C	A	A	C	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G	
A	T	C	A	T	C	A	A	C	A	C	C	A	G	C	A	T	G	C	A	A	G	A	C	C	T	G	C	A	C	G	

6/47

C - - - - -

Figure 3C

[illegible]

.....D

Figure 3D

C	T ₁₄₀	K	P	S	D	G ₁₄₅	N	C	T	C	I ₁₅₀	P	I
---	------------------	---	---	---	---	------------------	---	---	---	---	------------------	---	---

GTACAAACCTTCGGACGGAAAC
GTACAAACCTA C GGACGGAAAC
GTACAAACCTTCGGACGGAAAC
GTAC C AAACCTTCGGACGGAAAC
GTAC C AAACCTTCGGACGGAAAC
GTAC C AAACCTTCGGACGGAAAC
GTACAAACCTA C GGACGGAAAC
GTACAAACCTTCGGACGGAAAC
GTACAAACCTTCGGACGGAAAC
GTAC C AAACCTTCGGACGGAAAC
GTAC C AAACCTTCGGACGGAAAC
GTACAAACCTA C GGACGGAAAC
GTACAAACCTTCGGACGGAAAC

.....

Figure 3E

P	S	S	W	A	F	A	R ₁₆₀	F	L	W	E ₁₆₄	W																									
C	C	A	T	C	T	T	G	G	C	A	A	G	A	T	T	C	C	T	A	T	G	G	G	A	G	T	G	G									
C	C	A	T	C	A	T	C	T	T	T	C	G	C	A	A	A	T	A	C	C	T	A	T	G	G	G	A	G	T	G	G						
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	G	A	T	T	C	C	T	A	T	G	G	G	A	G	T	G	G					
C	C	A	T	C	A	T	C	T	G	G	G	C	T	T	T	C	G	A	A	A	T	T	C	C	T	A	T	G	G	G	A	G	T	G	G		
C	C	A	T	C	A	T	C	T	T	T	C	G	G	C	T	T	C	G	A	A	A	T	T	C	C	T	A	T	G	G	G	A	G	T	G	G	
C	C	A	T	C	A	T	C	T	T	T	C	G	G	C	T	T	C	G	A	A	A	T	T	C	C	T	A	T	G	G	G	A	G	T	G	G	
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A	T	C	A	T	C	T	C	T	G	G	C	A	A	A	T	A	C	C	C	T	A	T	G	G	G	A	G	T	G	G	A	G	T	G	G
C	C	A</																																			

*329616/HPBADRICG
221499/HPBADW3
221500/HPBCG
62280/XXHEPAV
59439/HBVAYWE
59429/HBVAYWC
59418/HBVADW2
59408/HBVADRM
59404/HBVADR4
329640/HPBAYW
313780/HBVAYWMCG
229417/HPBADW1

.....

Figure 3F

A	S	V	R	F ₁₇₀	S	W	L	S	L	V	P
---	---	---	---	------------------	---	---	---	---	---	---	---

*329616/HPBADR1CG

221499/HPBADW3

221500/HPBCG

62280/XXHEP AV

59439/HBVAYWE

59429/HBV/AYWC

59418/HBVADW2

59408/HBV/ADRM

59404/HBV/ADR4

329640/HPBAYW

313780/HBVAYWMC

229417/HPBADWI

G C C T C A G T C C G T T T C T C C T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G T C C G T T T C T C T T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G T C C G T T T C T C C T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G C C C G T T T C T C C T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G C C C G T T T C T C C T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G C C C G T T T C T C C T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G T C C G T T T C T C T T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G T C C G T T T C T C C T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G T C C G T T T C T C C T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G C C C G T T T C T C C T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G C C C G T T T C T C C T G G C T C A G T T T A C T A G T G C C A T
G C C T C A G T C C G T T T C T C T T G G C T C A G T T T A C T A G T G C C A T

10/47

.....G

Figure 3G

Figure 3H



S₁₉₃ V₁₉₄ I₁₉₅ W₁₉₆ M₁₉₇ M₁₉₈ W₁₉₉ Y₂₂₀ W G P S L

***329616/HPBADR1CG**

221499/HPBADW3

221500/HPBCG

62280/XXHEP AV

59439/HBVAYWE

59429/HBVAYWC

59418/HBVADW2

59408/HBV/ADRM

59404/HBV/ADR4

329640/HPBAYW

313780/HBVAYWMSG

229417/HPBADWI

[illegible]

12/47

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Figure 31

Figure 3J

[illegible]

*329616/HPBADRICG
221499/HPBADW3
221500/HPBCG
62280/XXHEPAV
59439/HBVAYWE
59429/HBVAYWC
59418/HBVADW2
59408/HBVADRM
59404/HBVADR4
329640/HPBAYW
313780/HBVAYWMCG
229417/HPBADW1

Figure 3K



pBBHBV1.28

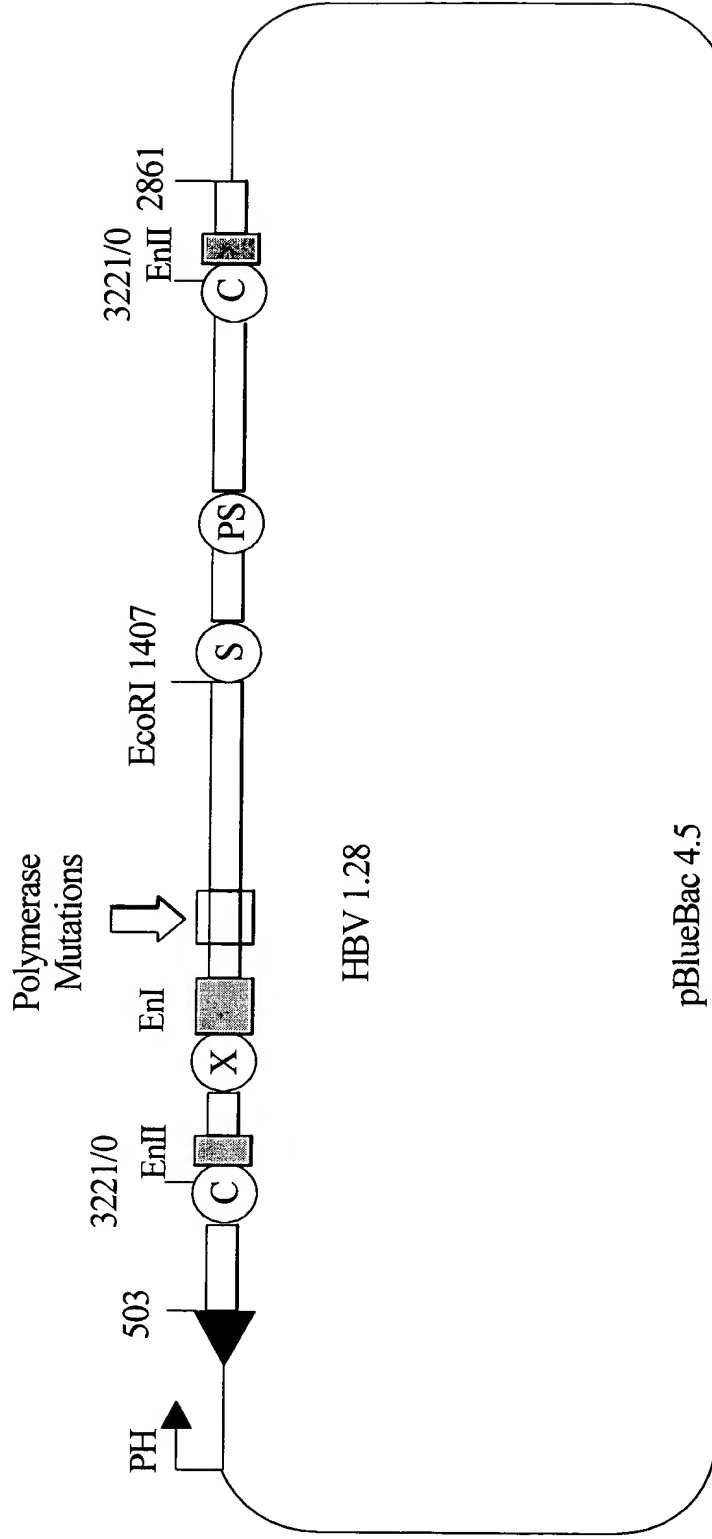
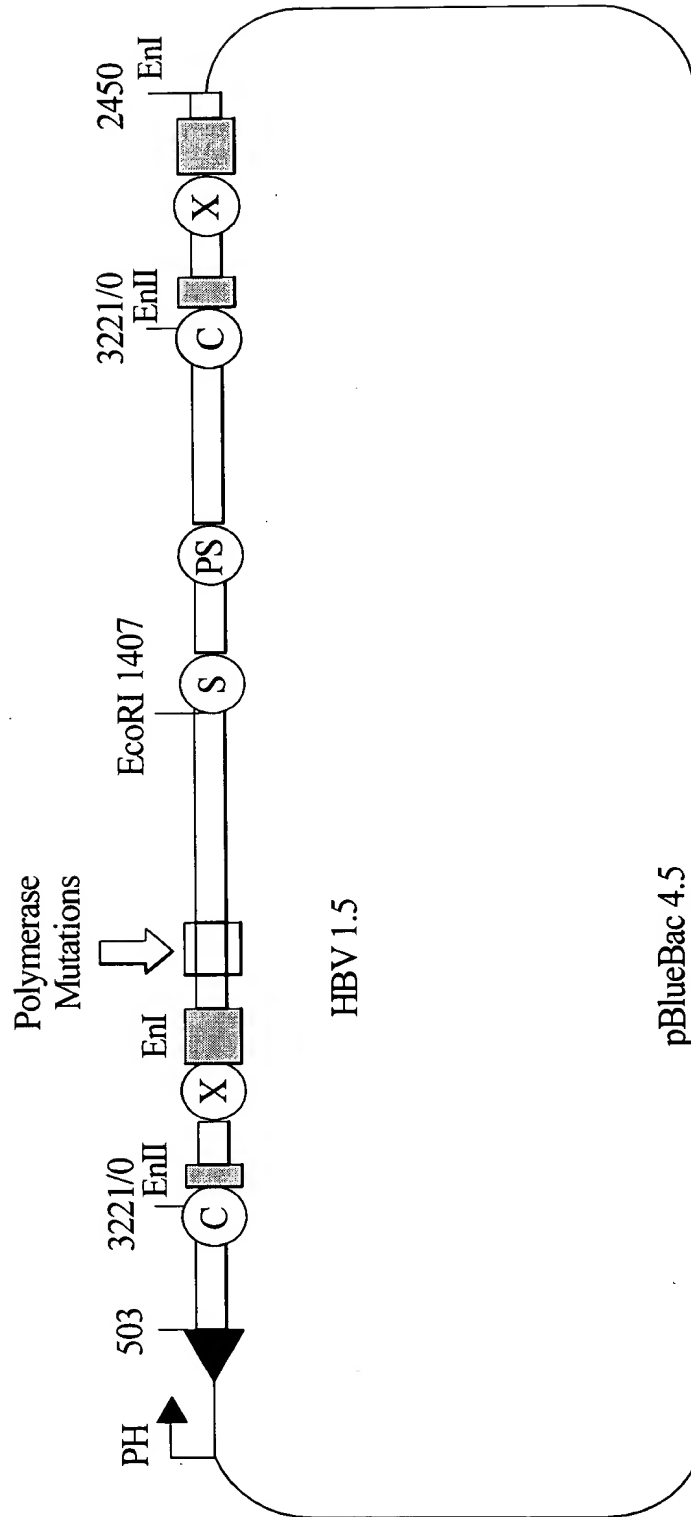


Figure 4A



042904



pBBHBV1.5

Figure 4B



Sequence Range: 1 to 4084

```
      10      20      30      40      50
GGACGACCCCTCGCGGGGCCGCTTGGGACTCTCTCGTCCCCTTCTCCGTC

      60      70      80      90     100
TGCCGTTCCAGCCGACCACGGGGCGCACCTCTCTTTACGCGGTCTCCCCG

     110     120     130     140     150
TCTGTGCCTTCTCATCTGCCGGTCCGTGTGCACTTCGCTTCACCTCTGCA

     160     170     180     190     200
CGTTGCATGGAGACCACCGTGAACGCCCATCAGATCCTGCCCAAGGTCTT

     210     220     230     240     250
ACATAAGAGGACTCTTGGACTCCCAGCAATGTCAACGACCGACCTTGAGG

     260     270     280     290     300
CCTACTTCAAAGACTGTGTGTTTAAGGACTGGGAGGAGCTGGGGGAGGAG

     310     320     330     340     350
ATTAGGTTAAAGGTCTTTGTATTAGGAGGCTGTAGGCATAAATTGGTCTG

     360     370     380     390     400
CGCACCAGCACCATGCAACTTTTTACCTCTGCCTAATCATCTCTTGTAC

     410     420     430     440     450
ATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCTTGGGTGGCTTTGGGGCA

     460     470     480     490     500
TGGACATTGACCCTTATAAAGAATTTGGAGCTACTGTGGAGTTACTCTCG

     510     520     530     540     550
TTTTTGCCTTCTGACTTCTTTCCTTCGTCAGAGATCTCCTAGACACCGC

     560     570     580     590     600
CTCAGCTCTGTATCGAGAAGCCTTAGAGTCTCCTGAGCATTGCTCACCTC

     610     620     630     640     650
ACCATACTGCACTCAGGCAAGCCATTCTCTGCTGGGGGGAATTGATGACT

     660     670     680     690     700
CTAGCTACCTGGGTGGGTAATAATTTGGAAGATCCAGCATCCAGGGATCT
```

A-----A

Figure 5A



A-----**A**

710 720 730 740 750
AGTAGTCAATTATGTTAATACTAACATGGGTTTAAAGATCAGGCAACTAT

760 770 780 790 800
TGTGGTTTCATATATCTTGCCTTACTTTTGGGAAGAGAGACTGTACTTGAA

810 820 830 840 850
TATTTGGTCTCTTTCGGAGTGTGGATTTCGCACTCCTCCAGCCTATAGACC

860 870 880 890 900
ACCAAATGCCCTATCTTATCAACACTTCCGGAACTACTGTTGTTAGAC

910 920 930 940 950
GACGGGACCGAGGCAGGTCCCCTAGAAGAAGAACTCCCTCGCCTCGCAGA

960 970 980 990 1000
CGCAGATCTCAATCGCCGCGTCGCAGAAGATCTCAATCTCGGGAATCTCA

1010 1020 1030 1040 1050
ATGTTAGTATTCCTTGGACTCATAAGGTGGGAACTTTACGGGGCTTTAT

1060 1070 1080 1090 1100
TCCTCTACAGTACCTATCTTTAATCCTGAATGGCAAACCTCCTTCCTTTCC

1110 1120 1130 1140 1150
TAAGATTCATTTACAAGAGGACATTATTAATAGGTGTCAACAATTTGTGG

1160 1170 1180 1190 1200
GCCCTCTCACTGTAAATGAAAAGAGAAGATTGAAATTAATTATGCCTGCT

1210 1220 1230 1240 1250
AGATTCTATCCTACCCACACTAAATATTTGCCCTTAGACAAAGGAATTAA

1260 1270 1280 1290 1300
ACCTTATTATCCAGATCAGGTAGTTAATCATTACTTCCAAACCAGACATT

1310 1320 1330 1340 1350
ATTTACATACTCTTTGGAAGGCTGGTATTCTATATAAGAGGGAAACCACA

1360 1370 1380 1390 1400
CGTAGCGCATCATTTTGGGGTCACCATATTCTTGGGAACAAGAGCTACA

1410 1420 1430 1440 1450
GCATGGGAGGTTGGTCATCAAAACCTCGCAAAGGCATGGGGACGAATCTT

B-----**B**

Figure 5B



B-----**B**

1460 1470 1480 1490 1500
TCTGTTCCCAACCCTCTGGGATTCTTTCCCGATCATCAGTTGGACCCTGC

1510 1520 1530 1540 1550
ATTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCATCAAGG

1560 1570 1580 1590 1600
ACCACTGGCCAGCAGCCAACCAGGTAGGAGTGGGAGCATTTCGGGCCAGGG

1610 1620 1630 1640 1650
CTCACCCCTCCACACGGCGGTATTTTGGGGTGGAGCCCTCAGGCTCAGGG

1660 1670 1680 1690 1700
CATATTGACCACAGTGTCAACAATTCCTCCTGCCTCCACCAATCGGC

1710 1720 1730 1740 1750
AGTCAGGAAGGCAGCCTACTCCCATCTCTCCACCTCTAAGAGACAGTCAT

1760 1770 1780 1790 1800
CCTCAGGCCATGCAGTGAATTCCACTGCCTTCCACCAAGCTCTGCAGGA

1810 1820 1830 1840 1850
TCCCAGAGTCAGGGGTCTGTATCTTCCTGCTGGTGGCTCCAGTTCAGGAA

1860 1870 1880 1890 1900
CAGTAAACCCTGCTCCGAATATTGCCTCTCACATCTCGTCAATCTCCGCG

1910 1920 1930 1940 1950
AGGACTGGGGACCCTGTGACGAACATGGAGAACATCACATCAGGATTCT

1960 1970 1980 1990 2000
AGGACCCCTGCTCGTGTTACAGGCGGGGTTTTCTTGTTGACAAGAATCC

2010 2020 2030 2040 2050
TCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAATTTTCTA

2060 2070 2080 2090 2100
GGGGGATCTCCCGTGTGTCTTGGCCAAAATTCGCAGTCCCCAACCTCCAA

2110 2120 2130 2140 2150
TCACTACCAACCTCCTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGT

2160 2170 2180 2190 2200
GTCTGCGGCGTTTTATCATATTCTCCTTCATCCTGCTGCTATGCCTCATC

C-----**C**

Figure 5C



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20/47

C-----C

2210 2220 2230 2240 2250
TTCTTATTGGTTCTTCTGGATTATCAAGGTATGTTGCCCGTTTGTCTCT

2260 2270 2280 2290 2300
AATTCAGGATCAACAACAACCAGTACGGGACCATGCAAAACCTGCACGA

2310 2320 2330 2340 2350
CTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTTGCTGTACAAAACCT

2360 2370 2380 2390 2400
ACGGATGGAAATTGCACCTGTATTCCCATCCCATCGTCCTGGGCTTTCGC

2410 2420 2430 2440 2450
AAAATACCTATGGGAGTGGGCCTCAGTCCGTTTCTCTTGGCTCAGTTTAC

2460 2470 2480 2490 2500
TAGTGCCATTTGTTTCAGTGGTTCGTAGGGCTTCCCCCACTGTTTGGCTT

2510 2520 2530 2540 2550
TCAGCTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAGCATCGT

2560 2570 2580 2590 2600
GAGTCCCTTTATACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACA

2610 2620 2630 2640 2650
TTTAAACCCTAACAAAACAAAAGATGGGGTTATTCCCTAAACTTCATGG

2660 2670 2680 2690 2700
GCTACATAATTGGAAGTTGGGGAACCTTGCCACAGGATCATATTGTACAA

2710 2720 2730 2740 2750
AAGATCAAACACTGTTTTAGAAAACCTCCTGTTAACAGGCCTATTGATTG

2760 2770 2780 2790 2800
GAAAGTATGTCAAAGAATTGTGGGTCTTTTGGGCTTGCTGCTCCATTTA

2810 2820 2830 2840 2850
CACAATGTGGATATCCTGCCTTAATGCCTTTGTATGCATGTATACAAGCT

2860 2870 2880 2890 2900
AAACAGGCTTTCACCTTCTCGCCAACCTTACAAGGCCTTCTAAGTAAACA

2910 2920 2930 2940 2950
GTACATGAACCTTTACCCCGTTGCTCGGCAACGGCCTGGTCTGTGCCAAG

D-----D

Figure 5D



042904

21/47

D-----D

2960 2970 2980 2990 3000
TGTTTGCTGACGCAACCCCCACTGGCTGGGGCTTGGCCATAGGCCATCAG

3010 3020 3030 3040 3050
CGCATGCGTGGAACCTTTGTGGCTCCTCTGCCGATCCATACTGCGGAACT

3060 3070 3080 3090 3100
CCTAGCCGCTTGTTTTGCTCGCAGCCGGTCTGGAGCAAAGCTCATCGGAA

3110 3120 3130 3140 3150
CTGACAATTCTGTCTCCTCTCGCGGAAATATACATCGTTTCCATGGCTG

3160 3170 3180 3190 3200
CTAGGCTGTACTGCCAACTGGATCCTTCGCGGGACGTCCTTTGTTTACGT

3210 3220 3230 3240 3250
CCCGTCGGCGCTGAATCCCGCGGACGACCCCTCGCGGGGCCGCTTGGGAC

3260 3270 3280 3290 3300
TCTCTCGTCCCTTCTCCGTCTGCCGTTCCAGCCGACCACGGGGCGCACC

3310 3320 3330 3340 3350
TCTCTTTACGCGGTCTCCCCGTCTGTGCCTTCTCATCTGCCGGTCCGTGT

3360 3370 3380 3390 3400
GCACTTCGCTTACCTCTGCACGTTGCATGGAGACCACCGTGAACGCCCA

3410 3420 3430 3440 3450
TCAGATCCTGCCCAAGGTCTTACATAAGAGGACTCTTGGACTCCCAGCAA

3460 3470 3480 3490 3500
TGTC AACGACCGACCTTGAGGCCTACTTCAAAGACTGTGTGTTTAAGGAC

3510 3520 3530 3540 3550
TGGGAGGAGCTGGGGGAGGAGATTAGGTTAAAGGTCTTTGTATTAGGAGG

3560 3570 3580 3590 3600
CTGTAGGCATAAATTGGTCTGCGCACCAGCACCATGCAACTTTTTCACCT

3610 3620 3630 3640 3650
CTGCCTAATCATCTCTTGTACATGTCCCACTGTTCAAGCCTCCAAGCTGT

3660 3670 3680 3690 3700
GCCTTGGGTGGCTTTGGGGCATGGACATTGACCCTTATAAAGAATTTGGA

E-----E

Figure 5E



E - - - - - E

3710 3720 3730 3740 3750
GCTACTGTGGAGTTACTCTCGTTTTGCCTTCTGACTTCTTTCCTTCCGT

3760 3770 3780 3790 3800
CAGAGATCTCCTAGACACCGCCTCAGCTCTGTATCGAGAAGCCTTAGAGT

3810 3820 3830 3840 3850
CTCCTGAGCATTGCTCACCTCACCATACTGCACTCAGGCAAGCCATTCTC

3860 3870 3880 3890 3900
TGCTGGGGGGAATTGATGACTCTAGCTACCTGGGTGGGTAATAATTTGGA

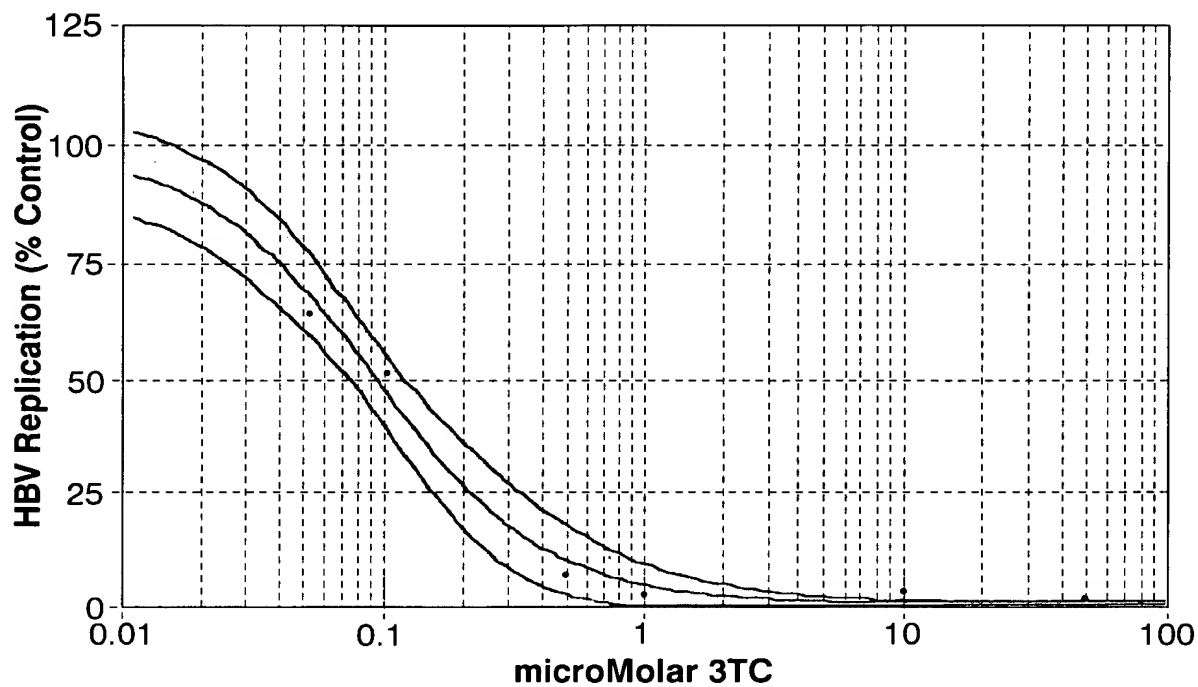
3910 3920 3930 3940 3950
AGATCCAGCATCCAGGGATCTAGTAGTCAATTATGTTAATACTAACATGG

3960 3970 3980 3990 4000
GTTTAAAGATCAGGCAACTATTGTGGTTTCATATATCTTGCCTTACTTTT

4010 4020 4030 4040 4050
GGAAGAGAGACTGTACTTGAATATTTGGTCTCTTTCGGAGTGTGGATTTCG

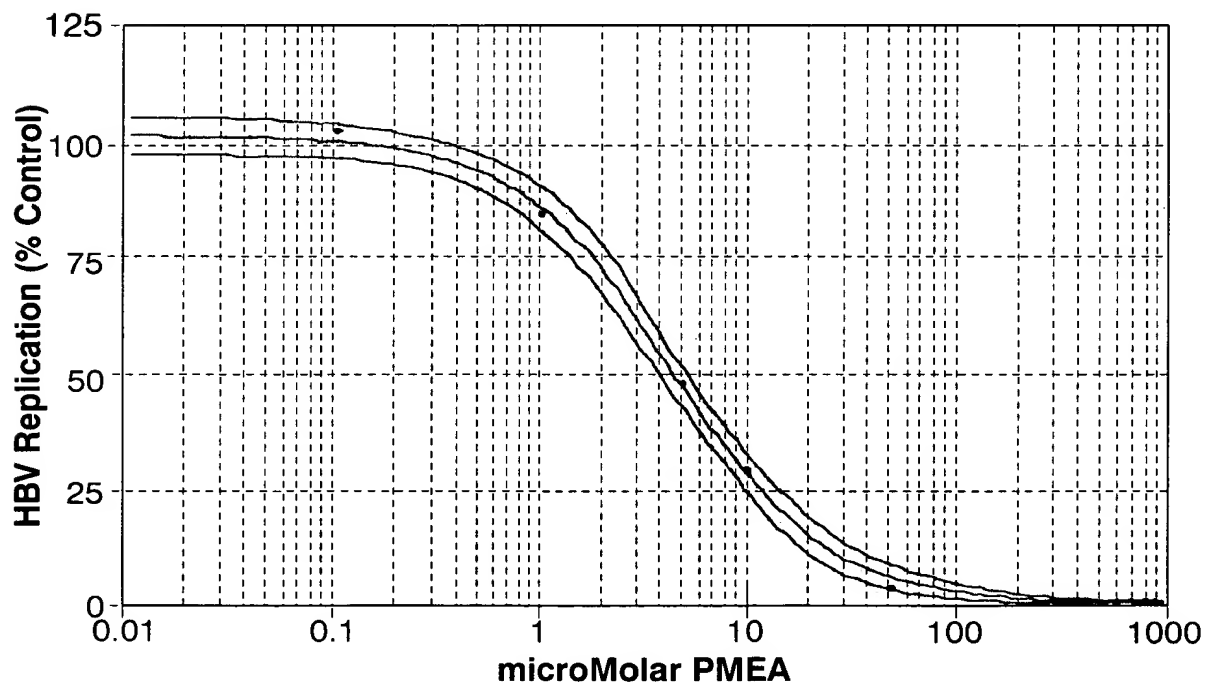
4060 4070 4080
CACTCCTCCAGCCTATAGACCACCAAATGCCCCT

Figure 5F



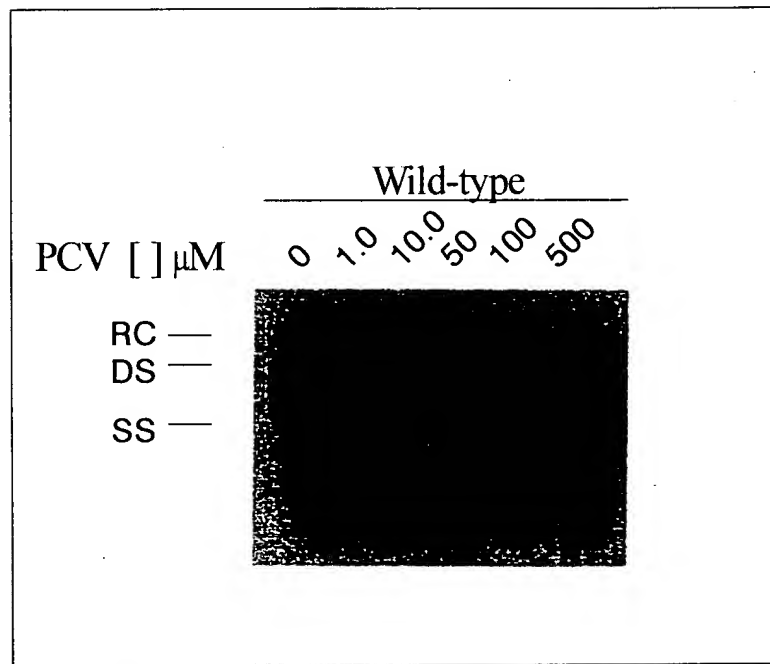
Rank 2 Eqn 8076 [LgstcDoseRsp_] $y = a / (1 + (x/b)^c)$

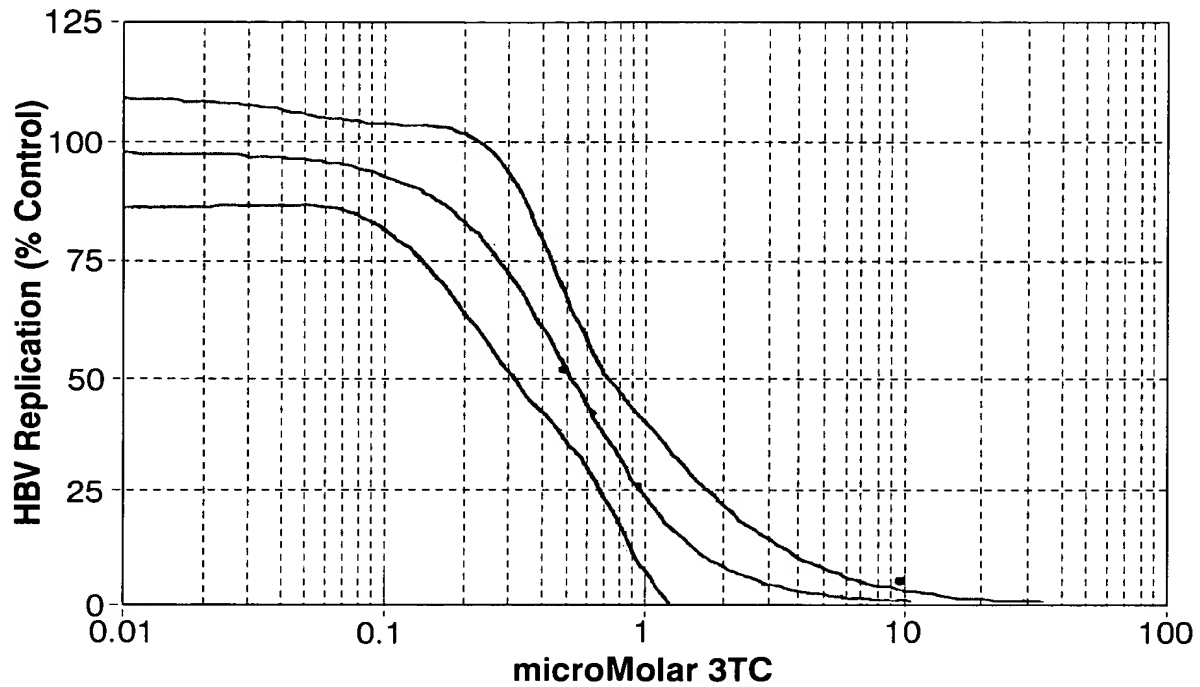
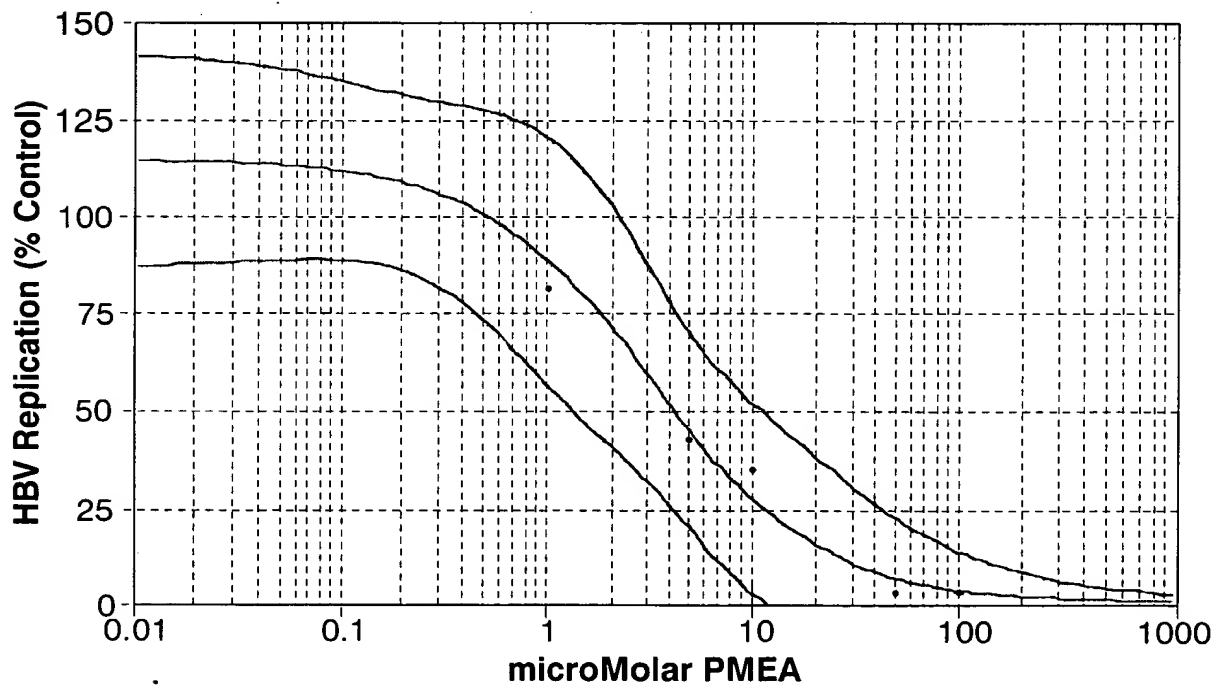
Figure 6A

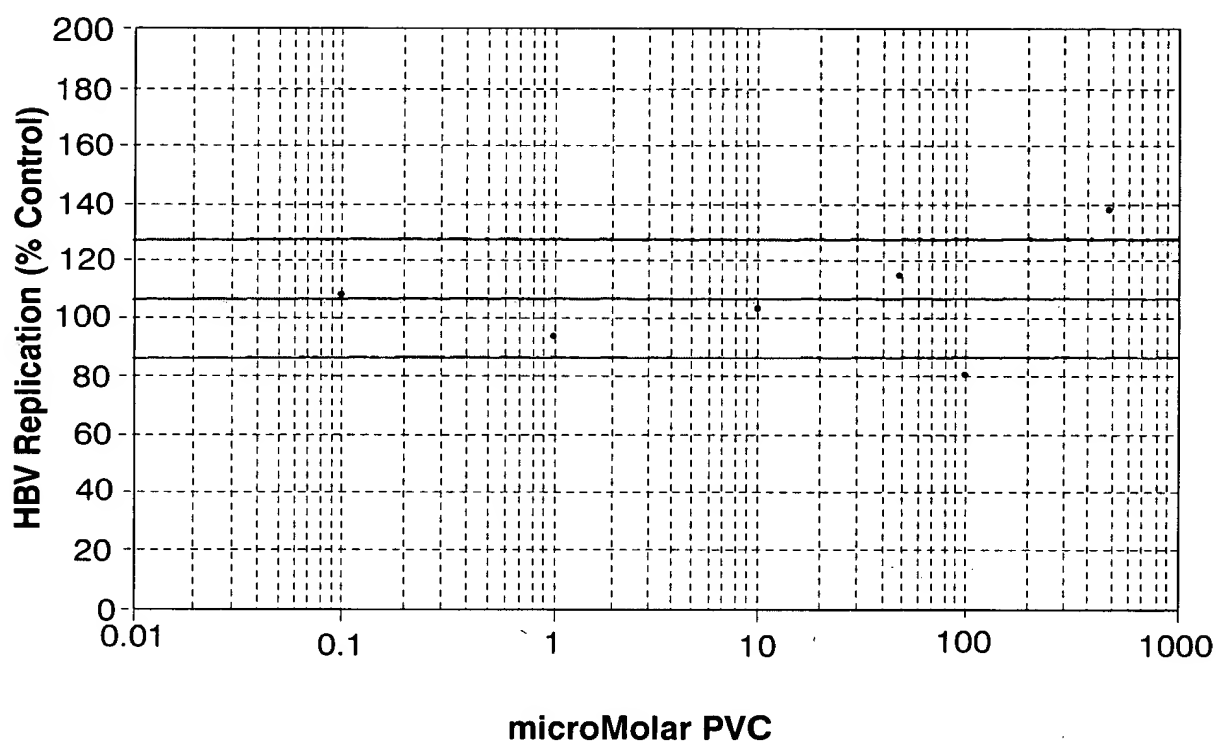


Rank 2 Eqn 8076 [LgstcDoseRsp_] $y = a / (1 + (x/b)^c)$

Figure 6B

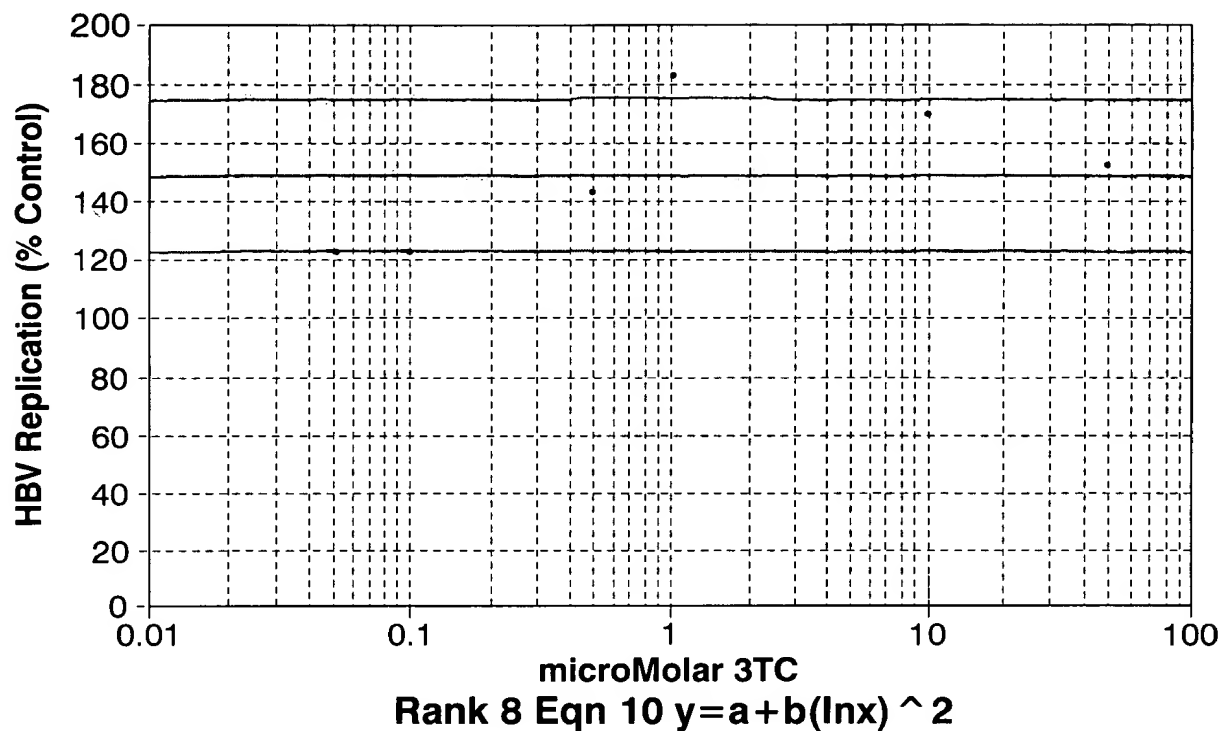
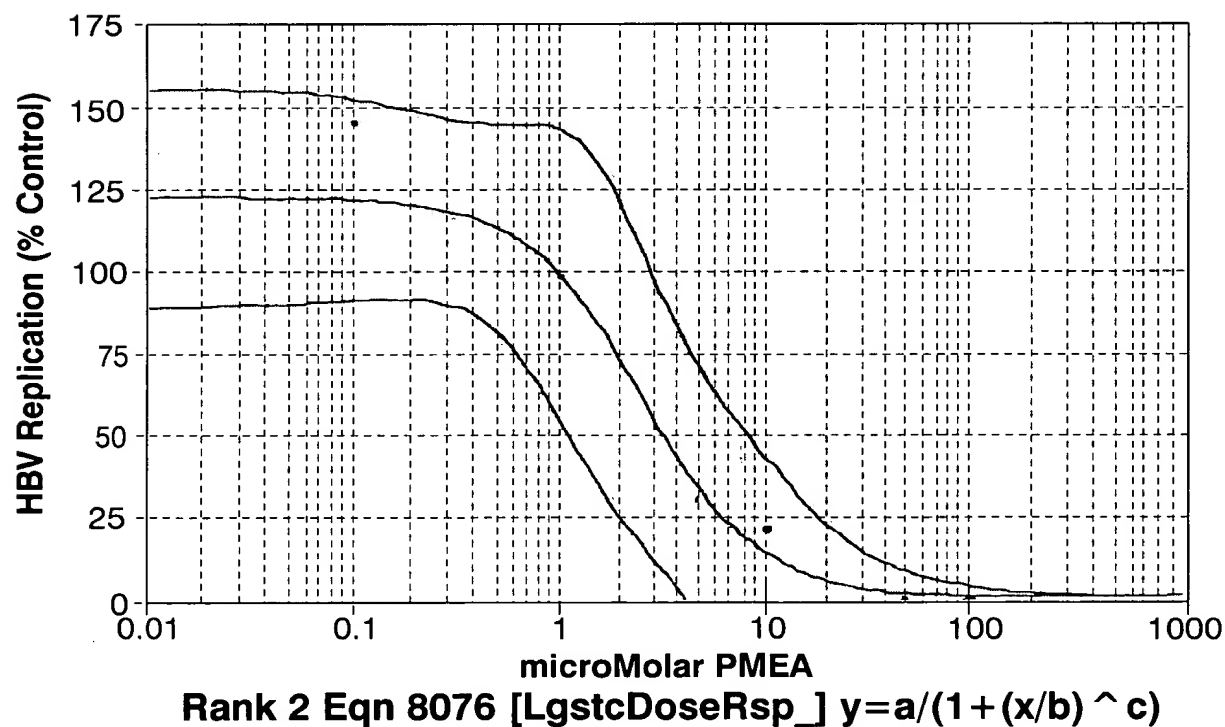
**Figure 6C**

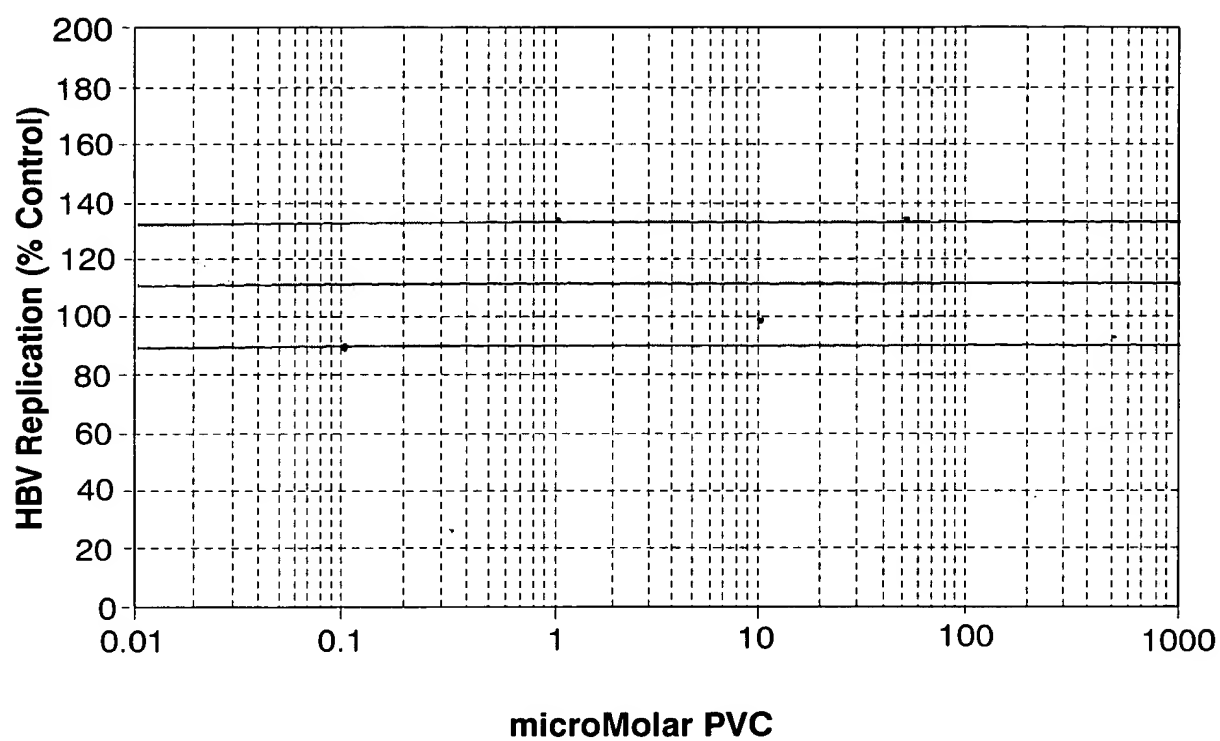
**Figure 7A****Figure 7B**



Rank 45 Eqn 19 $y=a+bx/x^2$

Figure 7C

**Figure 8A****Figure 8B**

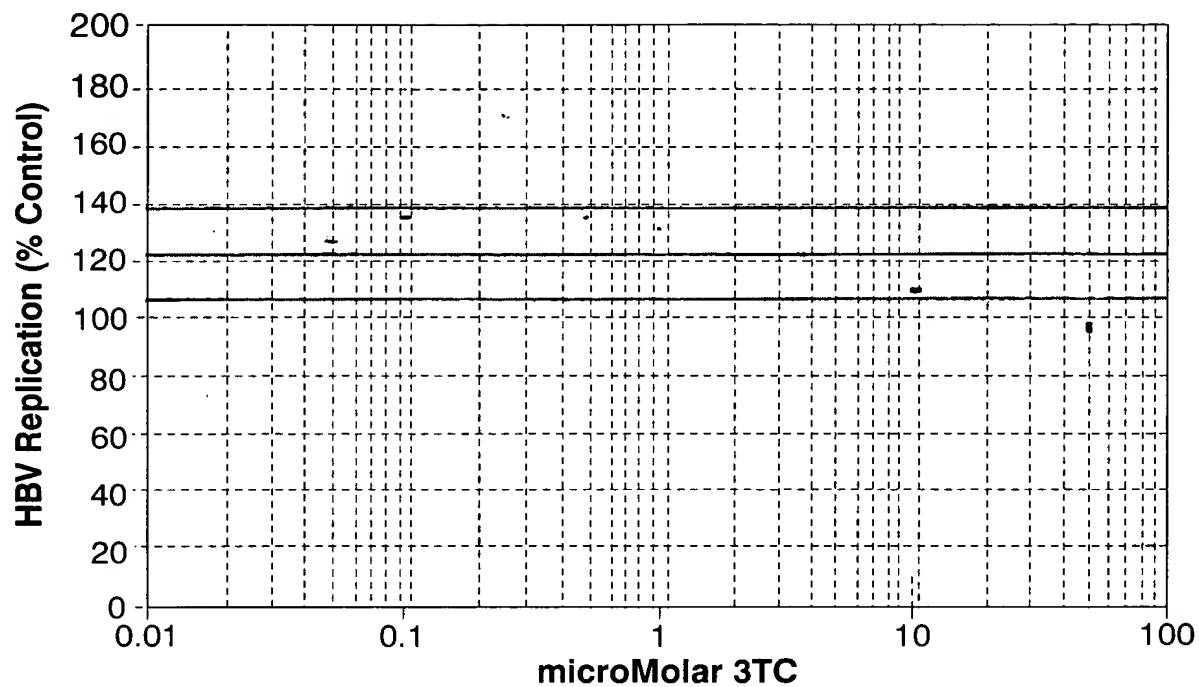
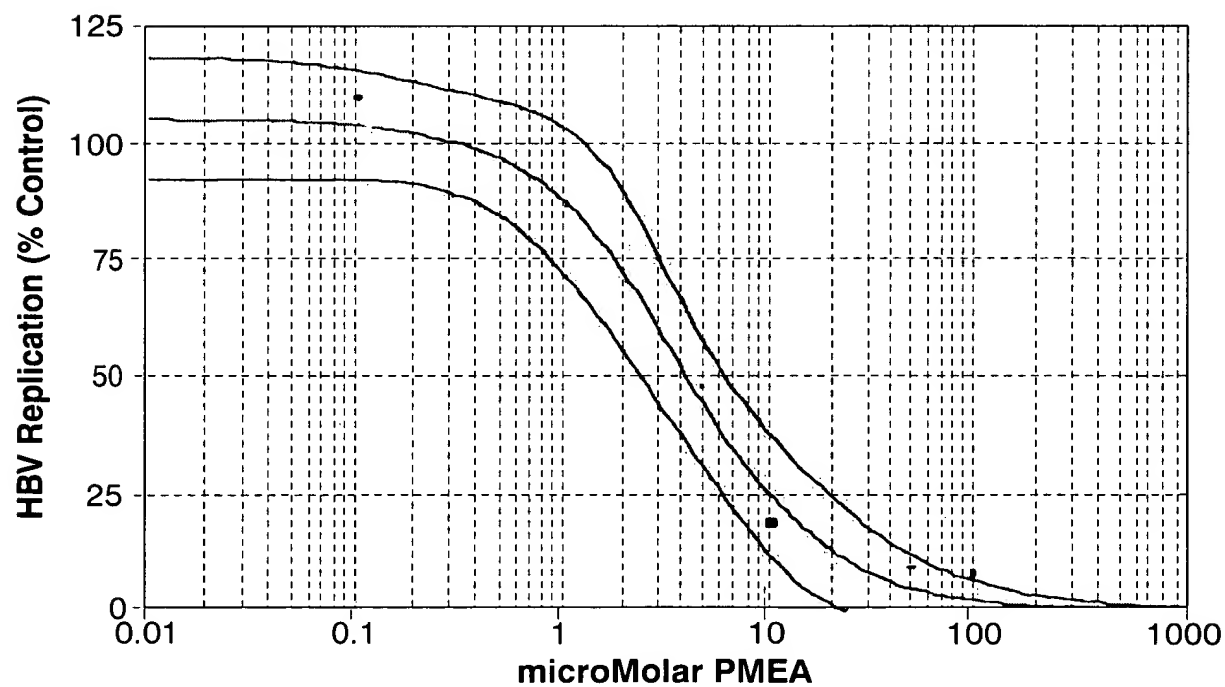


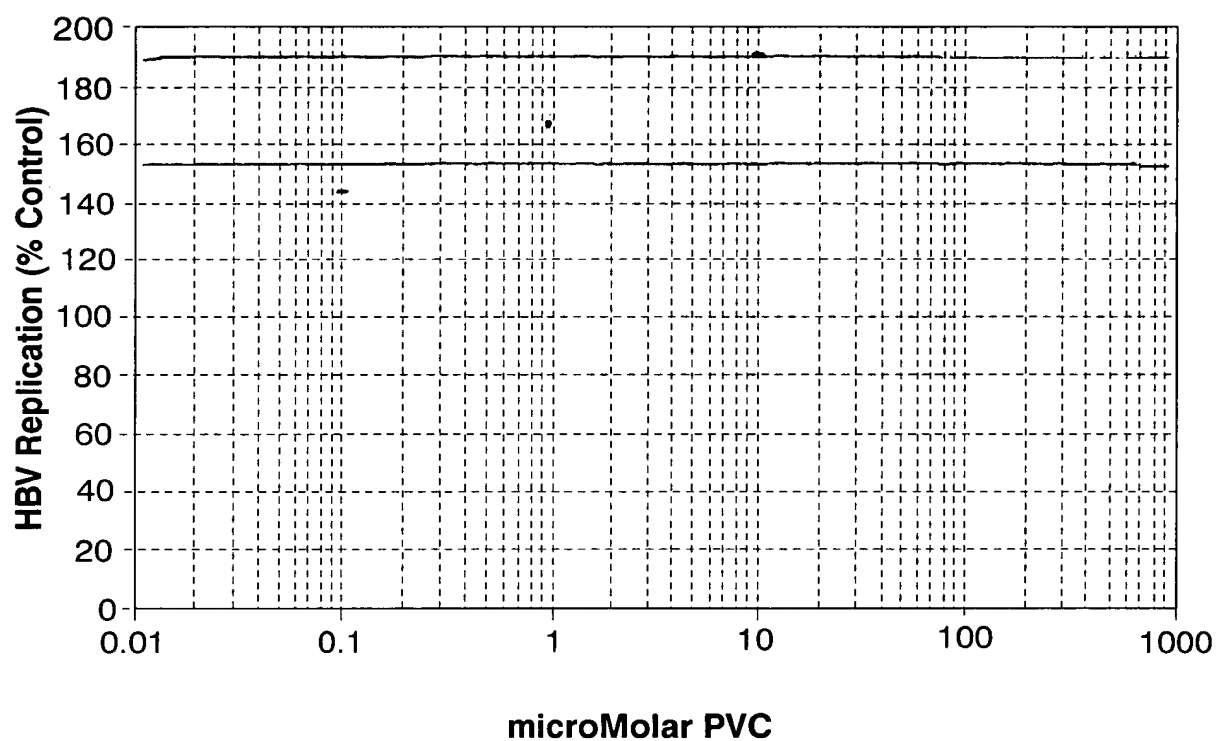
Rank 34 Eqn 10 $y=a+b(\ln x)^2$

Figure 8C



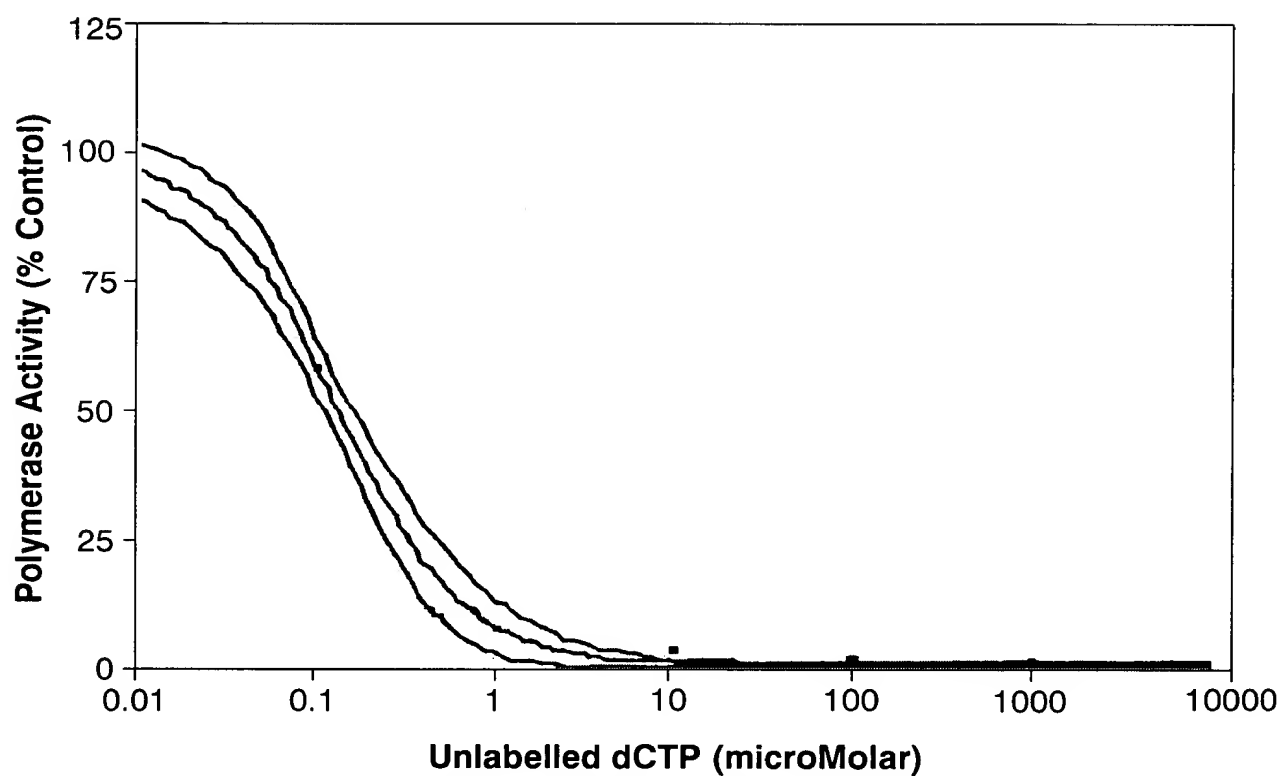
29/47

Rank 45 Eqn 10 $y=a+b(\ln x)^2$ **Figure 9A**Rank 2 Eqn 8076 $[LgstcDoseRsp_] y=a/(1+(x/b)^c)$ **Figure 9B**



Rank 20 Eqn 10 $y=a+b(\ln x)^2$

Figure 9C



Rank 2 Eqn 8076 [LgstcDoseRsp_] $y = a / (1 + (x/b)^c)$

Cold dCTP Competition

Figure 10



042904

32/47

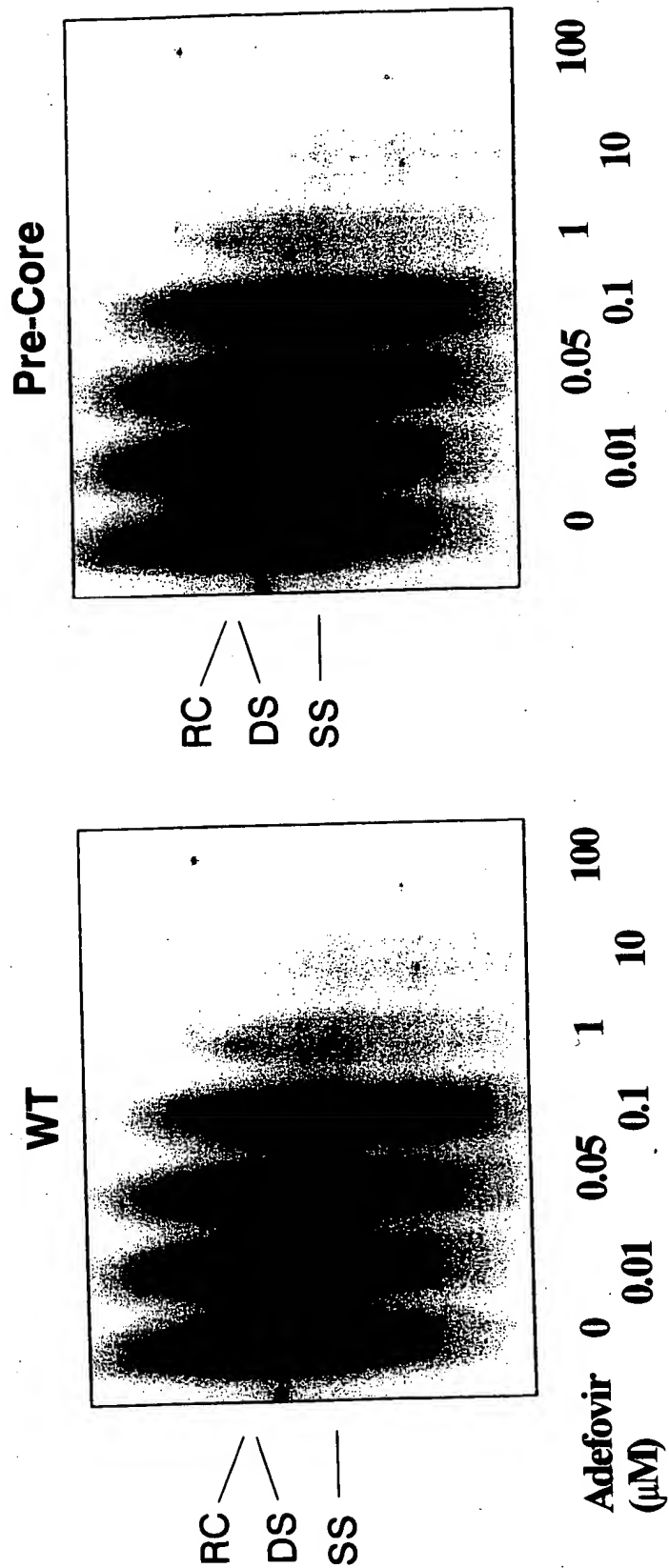


Figure 11A

Figure 11B

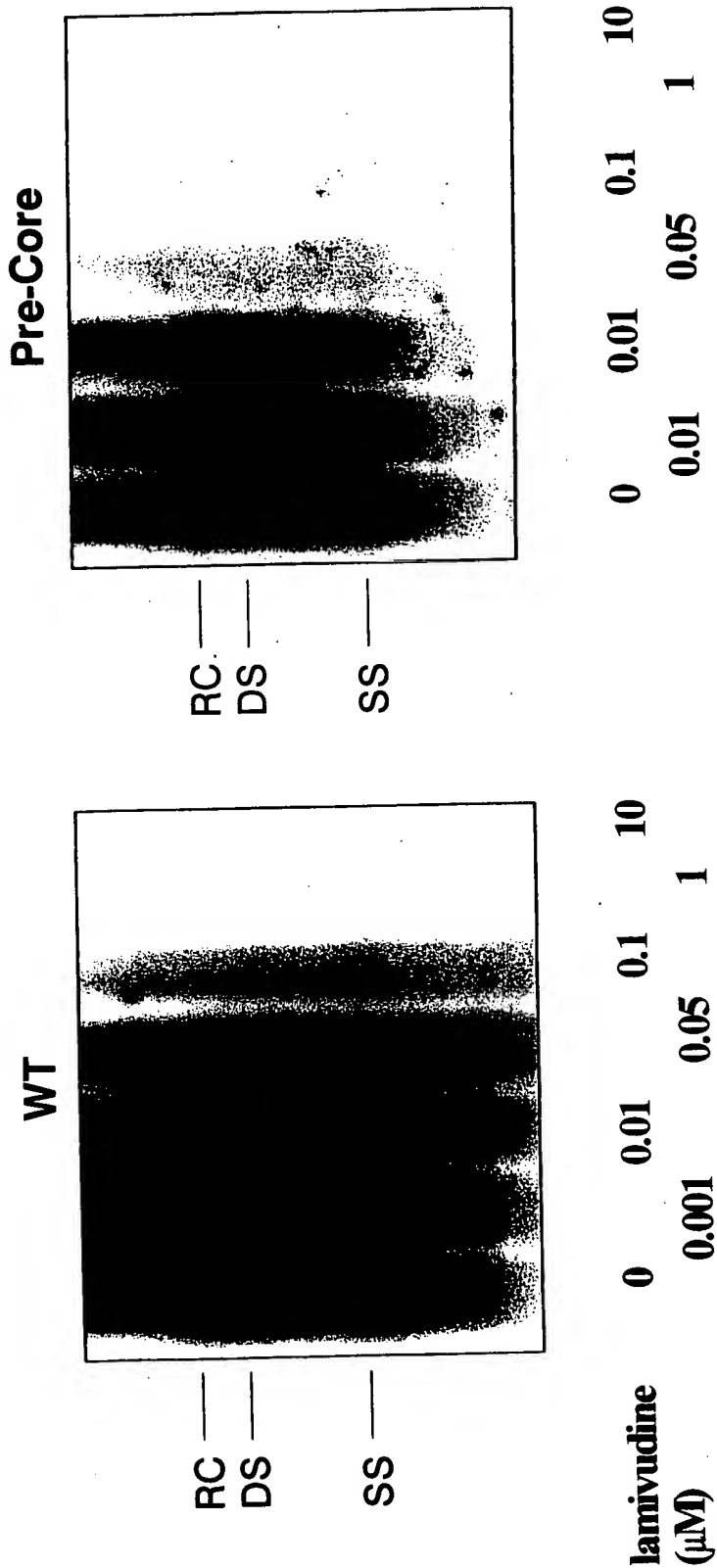


Figure 11D

Figure 11C



042904

34/47

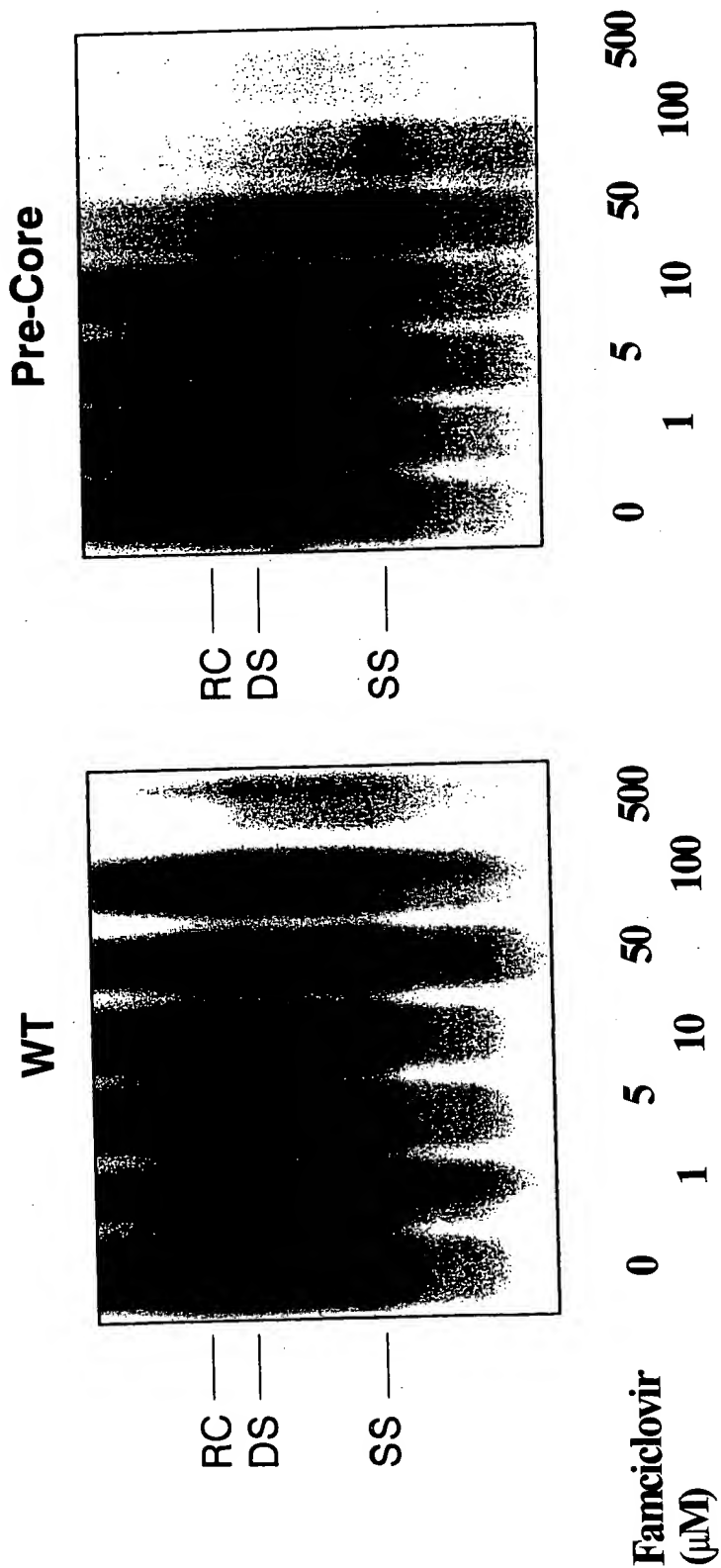


Figure 11F

Figure 11E

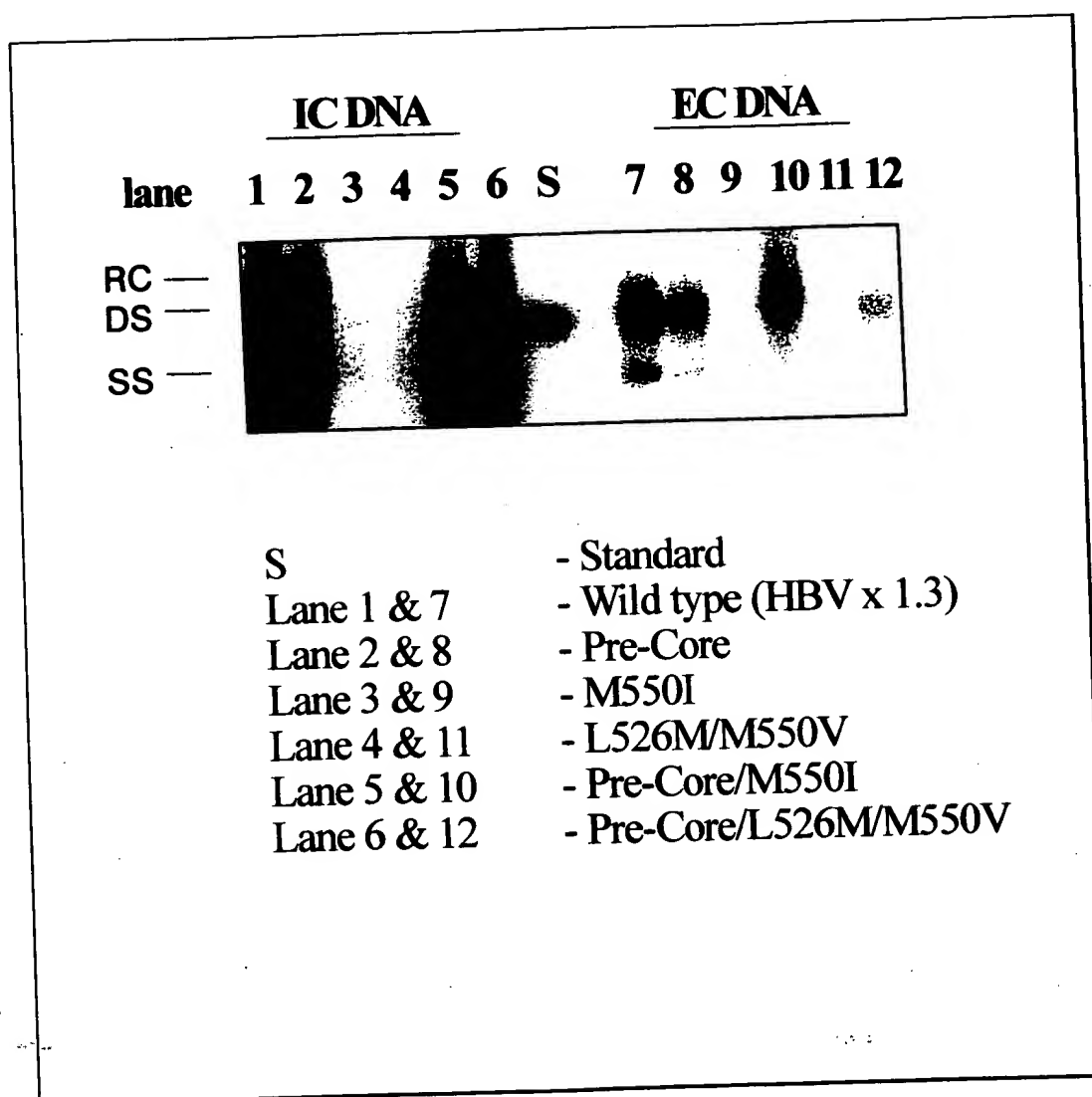


Figure 12

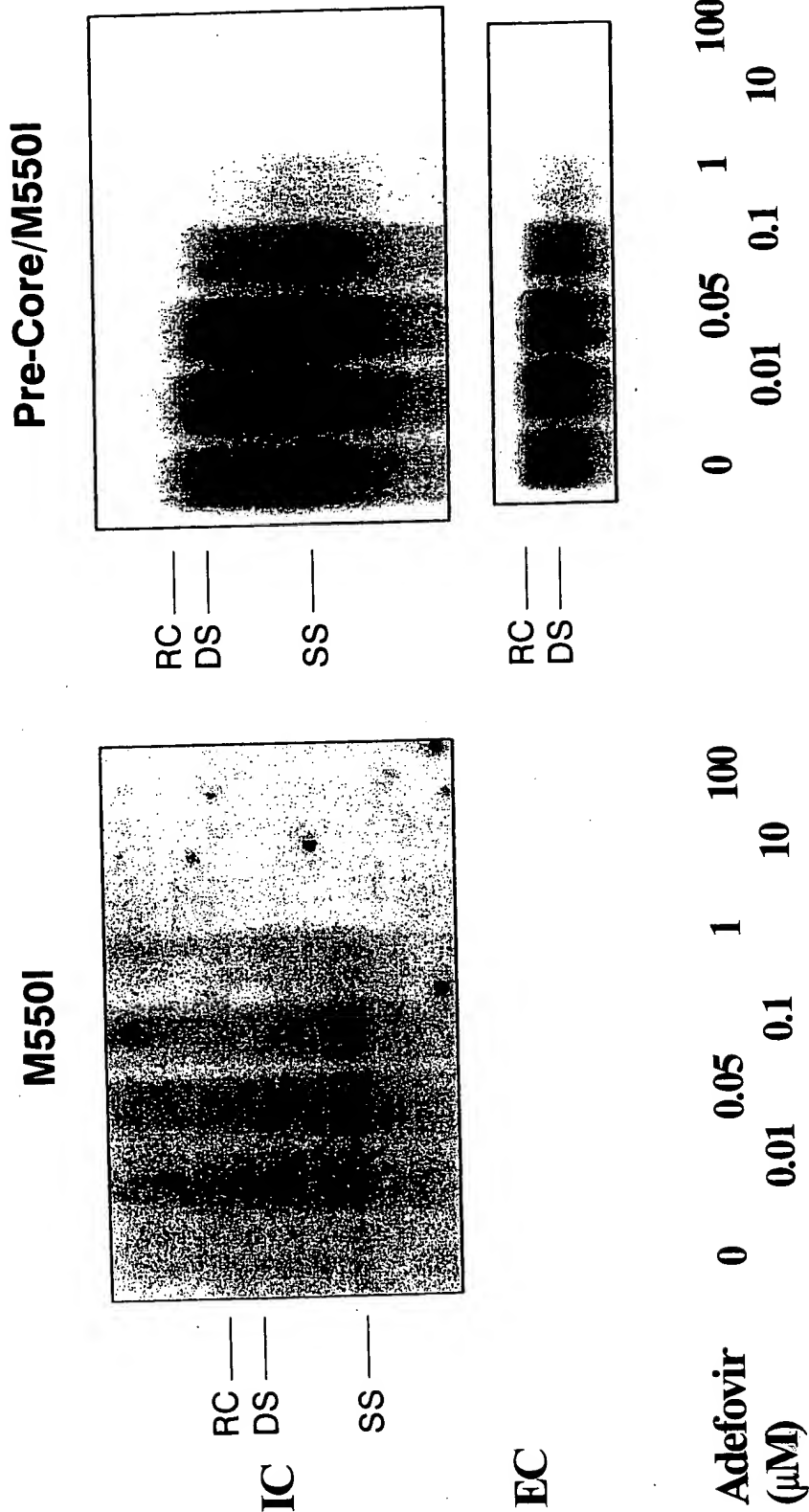
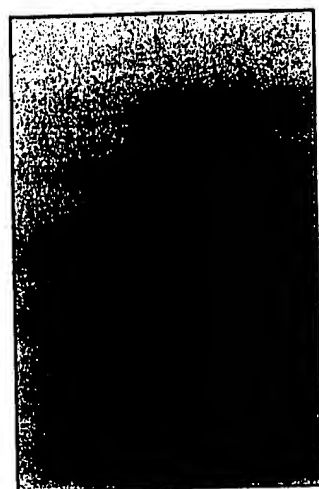


Figure 13B

Figure 13A



Pre-Core/L526M/M550V



0 0.01 0.05 1 10 100

Figure 13D

L526M/M550V



EC

Adefovir (μM) 0 0.01 0.05 1 10 100

Figure 13C

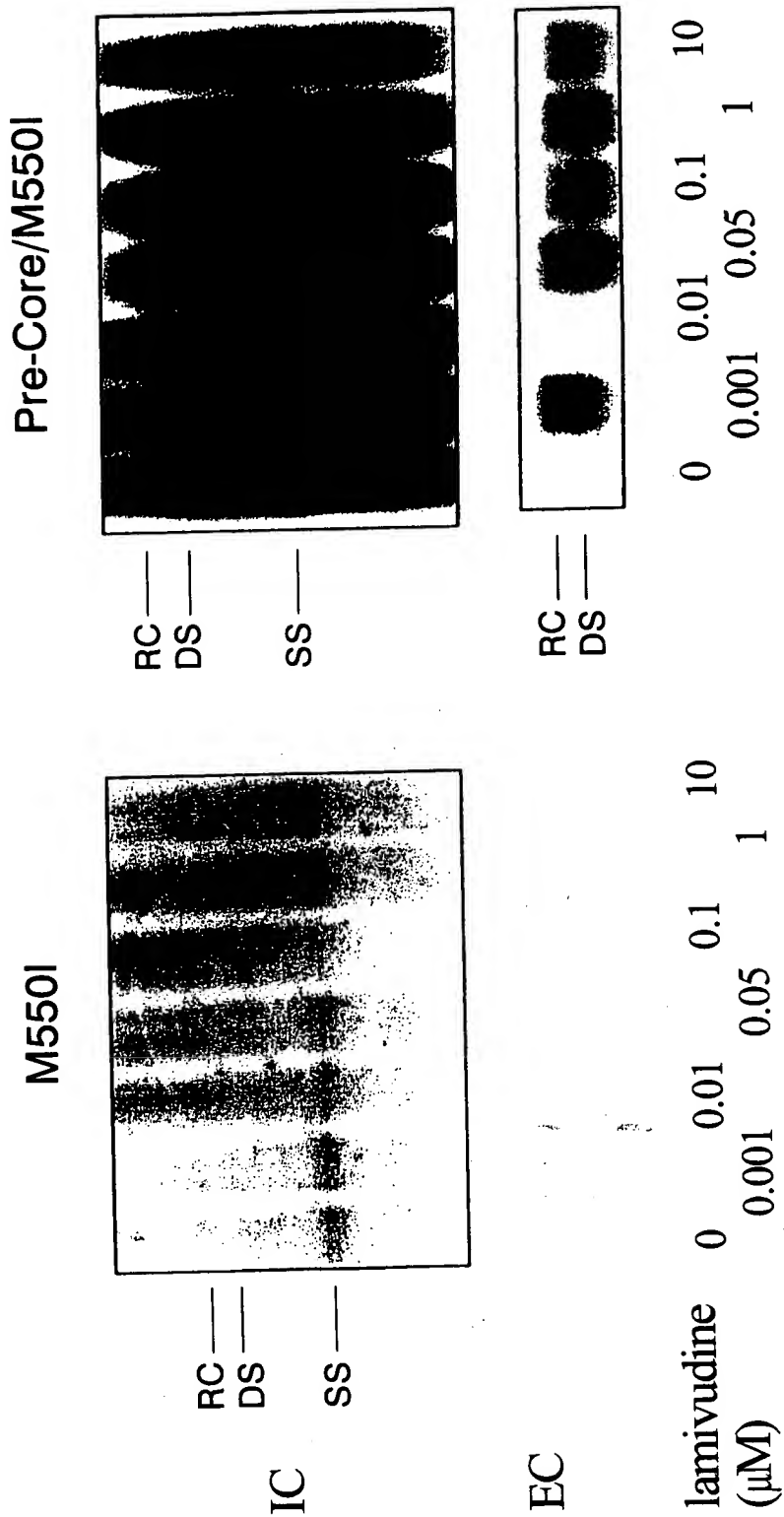
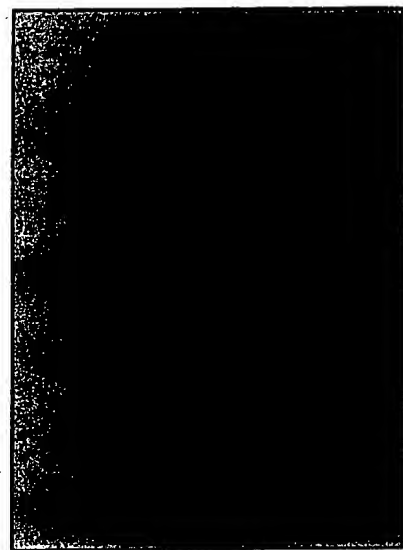


Figure 13F

Figure 13E



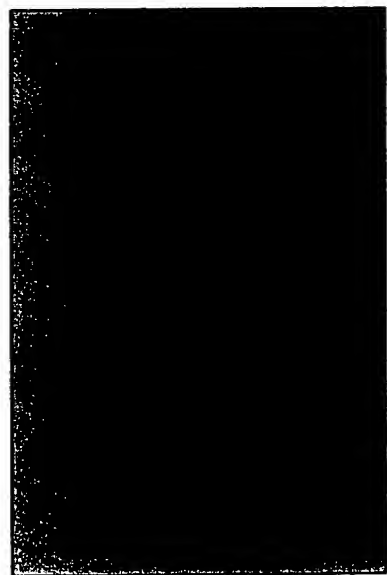
Pre-Core/L526M/M550V



0 0.001 0.01 0.1 10

Figure 13H

L526M/M550V



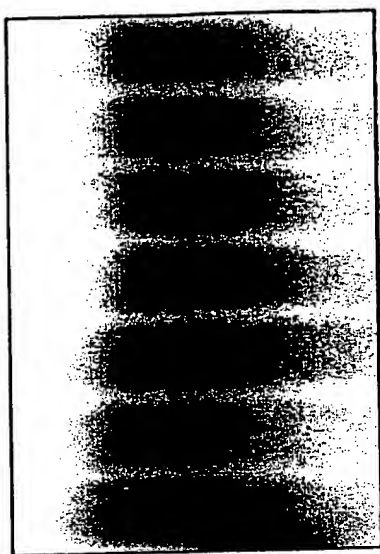
EC

lamivudine 0 0.001 0.01 0.1 10
(μ M) 0.05 1

Figure 13G



Pre-Core/M550I

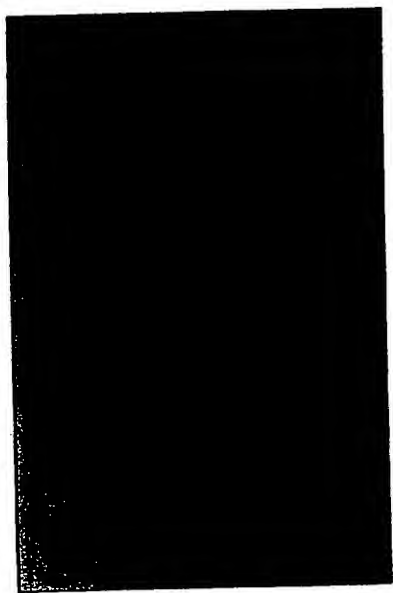


RC —
DS —
SS —

0 1 5 10 50 100 500

Figure 13J

M550I



RC —
DS —
SS —
IC

EC

Famciclovir 0 1 5 10 50 100 500
(μ M)

Figure 13I

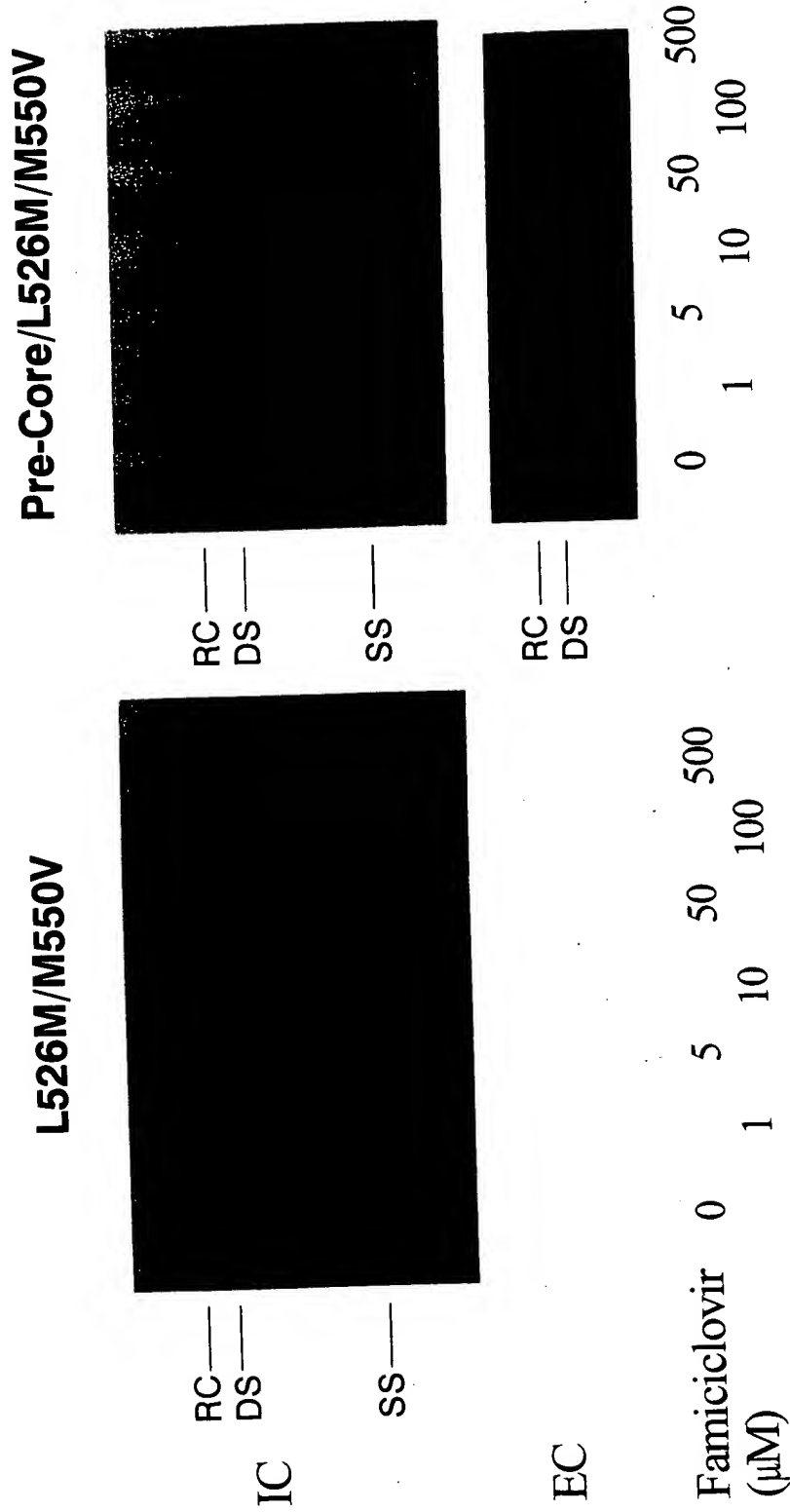


Figure 13L

Figure 13K



Sequence Range: 1 to 4496

```
      10      20      30      40      50
GATATCCTGCCTTAATGCCTTTGTATGCATGTATACAAGCTAAACAGGCT

      60      70      80      90     100
TTCACCTTTCTCGCCAACTTACAAGGCCTTTCTAAGTAAACAGTACATGAA

     110     120     130     140     150
CCTTTACCCCGTTGCTCGGCAACGGCCTGGTCTGTGCCAAGTGTTTGCTG

     160     170     180     190     200
ACGCAACCCCCACTGGCTGGGGCTTGGCCATAGGCCATCAGCGCATGCGT

     210     220     230     240     250
GGAACCTTTGTGGCTCCTCTGCCGATCCATACTGCGGAACTCCTAGCCGC

     260     270     280     290     300
TTGTTTTGCTCGCAGCCGGTCTGGAGCAAAGCTCATCGGAACTGACAATT

     310     320     330     340     350
CTGTCGTCCTCTCGCGGAAATATACATCGTTTCCATGGCTGCTAGGCTGT

     360     370     380     390     400
ACTGCCAACTGGATCCTTCGCGGGACGTCCTTTGTTTACGTCCCGTCGGC

     410     420     430     440     450
GCTGAATCCCGCGGACGACCCCTCGCGGGGCCGCTTGGGACTCTCTCGTC

     460     470     480     490     500
CCCTTCTCCGTCTGCCGTTCCAGCCGACCACGGGGCGCACCTCTCTTTAC

     510     520     530     540     550
GCGGTCTCCCCGTCTGTGCCTTCTCATCTGCCGGTCCGTGTGCACTTCGC

     560     570     580     590     600
TTCACCTCTGCACGTTGCATGGAGACCACCGTGAACGCCCATCAGATCCT

     610     620     630     640     650
GCCCAAGGTCTTACATAAGAGGACTCTTGGA CTCCCAGCAATGTCAACGA

     660     670     680     690     700
CCGACCTTGAGGCCTACTTCAAGACTGTGTGTTTAAGGACTGGGAGGAG
```

A-----A

Figure 14A



43/47

A-----A

710 720 730 740 750
CTGGGGGAGGAGATTAGGTTAAAGGTCTTTGTATTAGGAGGCTGTAGGCA

760 770 780 790 800
TAAATTGGTCTGCGCACCAGCACCATGCAACTTTTTCACCTCTGCCTAAT

810 820 830 840 850
CATCTCTTGATACATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCTTGGGT

860 870 880 890 900
GGCTTTGGGGCATGGACATTGACCCTTATAAAGAATTTGGAGCTACTGTG

910 920 930 940 950
GAGTTACTCTCGTTTTTGCCTTCTGACTTCTTTCCTTCCGTCAGAGATCT

960 970 980 990 1000
CCTAGACACCGCCTCAGCTCTGTATCGAGAAGCCTTAGAGTCTCCTGAGC

1010 1020 1030 1040 1050
ATTGCTCACCTCACCATACTGCACTCAGGCAAGCCATTCTCTGCTGGGGG

1060 1070 1080 1090 1100
GAATTGATGACTCTAGCTACCTGGGTGGGTAATAATTTGGAAGATCCAGC

1110 1120 1130 1140 1150
ATCCAGGGATCTAGTAGTCAATTATGTTAATACTAACATGGGTTTAAAGA

1160 1170 1180 1190 1200
TCAGGCAACTATTGTGGTTTCATATATCTTGCCTTACTTTTGGGAAGAGAG

1210 1220 1230 1240 1250
ACTGTACTTGAATATTTGGTCTCTTTCGGAGTGTGGATTTCGCACTCCTCC

1260 1270 1280 1290 1300
AGCCTATAGACCACCAAATGCCCCCTATCTTATCAACACTTCCGGAAACTA

1310 1320 1330 1340 1350
CTGTTGTTAGACGACGGGACCGAGGCAGGTCCCCCTAGAAGAAGAACTCCC

1360 1370 1380 1390 1400
TCGCCTCGCAGACGCAGATCTCAATCGCCGCGTCGCAGAAGATCTCAATC

1410 1420 1430 1440 1450
TCGGGAATCTCAATGTTAGTATTCCTTGGACTCATAAGGTGGGAACTTT

B-----B

Figure 14B



042904

44/47

B-----**B**

1460	1470	1480	1490	1500
ACGGGGCTTTATTCCTCTACAGTACCTATCTTTAATCCTGAATGGCAAAC				
1510	1520	1530	1540	1550
TCCTTCCTTTCCTAAGATTCATTACAAAGAGGACATTATTAATAGGTGTC				
1560	1570	1580	1590	1600
AACAAATTTGTGGGCCCTCTCACTGTAAATGAAAAGAGAAGATTGAAATTA				
1610	1620	1630	1640	1650
ATTATGCCTGCTAGATTCTATCCTACCCACACTAAATATTTGCCCTTAGA				
1660	1670	1680	1690	1700
CAAAGGAATTAAACCTTATTATCCAGATCAGGTAGTTAATCATTACTTCC				
1710	1720	1730	1740	1750
AAACCAGACATTATTTACATACTCTTTGGAAGGCTGGTATTCTATATAAG				
1760	1770	1780	1790	1800
AGGGAAACCACACGTAGCGCATCATTTTGCGGGTCACCATATTCTTGGA				
1810	1820	1830	1840	1850
ACAAGAGCTACAGCATGGGAGGTTGGTCATCAAAACCTCGCAAAGGCATG				
1860	1870	1880	1890	1900
GGGACGAATCTTTCTGTTCCCAACCCTCTGGGATTCTTTCCCGATCATCA				
1910	1920	1930	1940	1950
GTTGGACCTGCATTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCA				
1960	1970	1980	1990	2000
ACCCCATCAAGGACCACTGGCCAGCAGCCAACCAGGTAGGAGTGGGAGCA				
2010	2020	2030	2040	2050
TTCGGGCCAGGGCTCACCCCTCCACACGGCGGTATTTTGGGGTGGAGCCC				
2060	2070	2080	2090	2100
TCAGGCTCAGGGCATATTGACCACAGTGTCAACAATTCCTCCTCCTGCCT				
2110	2120	2130	2140	2150
CCACCAATCGGCAGTCAGGAAGGCAGCCTACTCCCATCTCTCCACCTCTA				
2160	2170	2180	2190	2200
AGAGACAGTCATCCTCAGGCCATGCAGTGGAATTCCACTGCCTTCCACCA				

-----**C**

Figure 14C



042904

45/47

C-----**C**

2210	2220	2230	2240	2250
AGCTCTGCAGGATCCCAGAGTCAGGGGTCTGTATCTTCCTGCTGGTGGCT				
2260	2270	2280	2290	2300
CCAGTTCAGGAACAGTAAACCCTGCTCCGAATATTGCCTCTCACATCTCG				
2310	2320	2330	2340	2350
TCAATCTCCGCGAGGACTGGGGACCCTGTGACGAACATGGAGAACATCAC				
2360	2370	2380	2390	2400
ATCAGGATTTCCTAGGACCCCTGCTCGTGTACAGGCGGGGTTTTTCTTGT				
2410	2420	2430	2440	2450
TGACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCT				
2460	2470	2480	2490	2500
CTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCAAAATTTCGAGTC				
2510	2520	2530	2540	2550
CCCAACCTCCAATCACTACCAACCTCCTGTCCTCCAATTTGTCCTGGTT				
2560	2570	2580	2590	2600
ATCGCTGGATGTGTCTGCGGCGTTTTATCATATTCCTCTTCATCCTGCTG				
2610	2620	2630	2640	2650
CTATGCCTCATCTTCTTATTGGTTCTTCTGGATTATCAAGGTATGTTGCC				
2660	2670	2680	2690	2700
CGTTTGTCTCTAATTCCAGGATCAACAACAACCAGTACGGGACCATGCA				
2710	2720	2730	2740	2750
AAACCTGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTTGC				
2760	2770	2780	2790	2800
TGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCATCCCATCGTC				
2810	2820	2830	2840	2850
CTGGGCTTTCGCAAAATACCTATGGGAGTGGGCCTCAGTCCGTTTCTCTT				
2860	2870	2880	2890	2900
GGCTCAGTTTACTAGTGCCATTTGTTTCAGTGGTTCGTAGGGCTTTCCCC				
2910	2920	2930	2940	2950
ACTGTTTGGCTTTCAGCTATATGGATGATGTGGTATTGGGGGCCAAGTCT				

D-----**D**

Figure 14D



042904

46/47

D-----**D**

2960	2970	2980	2990	3000
GTACAGCATCGTGAGTCCCTTTATACCGCTGTTACCAATTTTCTTTTGTC				
3010	3020	3030	3040	3050
TCTGGGTATACATTTAAACCCTAACAAAACAAAAGATGGGGTTATTCCC				
3060	3070	3080	3090	3100
TAAACTTCATGGGCTACATAATTGGAAGTTGGGGAACCTTGCCACAGGAT				
3110	3120	3130	3140	3150
CATATTGTACAAAAGATCAAACACTGTTTTAGAAAACCTTCCTGTTAACAG				
3160	3170	3180	3190	3200
GCCTATTGATTGGAAAGTATGTCAAAGAATTGTGGGTCTTTTGGGCTTTG				
3210	3220	3230	3240	3250
CTGCTCCATTTACACAATGTGGATATCCTGCCTTAATGCCTTTGTATGCA				
3260	3270	3280	3290	3300
TGTATACAAGCTAAACAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTT				
3310	3320	3330	3340	3350
TCTAAGTAAACAGTACATGAACCTTTACCCCGTTGCTCGGCAACGGCCTG				
3360	3370	3380	3390	3400
GTCTGTGCCAAGTGTTTGCTGACGCAACCCCCACTGGCTGGGGCTTG GCC				
3410	3420	3430	3440	3450
ATAGGCCATCAGCGCATGCGTGGAACCTTTGTGGCTCCTCTGCCGATCCA				
3460	3470	3480	3490	3500
TACTGCGGAACCTCCTAGCCGCTTGTTTTGCTCGCAGCCGGTCTGGAGCAA				
3510	3520	3530	3540	3550
AGCTCATCGGAACCTGACAATTCTGTCGTCTCTCGCGGAAATATACATCG				
3560	3570	3580	3590	3600
TTTCCATGGCTGCTAGGCTGTACTGCCAACTGGATCCTTCGCGGGACGTC				
3610	3620	3630	3640	3650
CTTTGTTTACGTCCCGTCGGCGCTGAATCCCGCGGACGACCCCTCGCGGG				
3660	3670	3680	3690	3700
GCCGCTTGGGACTCTCTCGTCCCCTTCTCCGTCTGCCGTTCCAGCCGACC				

E-----**E**

Figure 14E



042904

47/47

E - - - - - E

3710 3720 3730 3740 3750
ACGGGGCGCACCTCTCTTTACGCGGTCTCCCCGTCTGTGCCTTCTCATCT

3760 3770 3780 3790 3800
GCCGGTCCGTGTGCACTTCGCTTCACCTCTGCACGTTGCATGGAGACCAC

3810 3820 3830 3840 3850
CGTGAACGCCCATCAGATCCTGCCCAAGGTCTTACATAAGAGGACTCTTG

3860 3870 3880 3890 3900
GACTCCCAGCAATGTCAACGACCGACCTTGAGGCCTACTTCAAAGACTGT

3910 3920 3930 3940 3950
GTGTTTAAGGACTGGGAGGAGCTGGGGGAGGAGATTAGGTTAAAGGTCTT

3960 3970 3980 3990 4000
TGTATTAGGAGGCTGTAGGCATAAATTGGTCTGCGCACGACCATGCA

4010 4020 4030 4040 4050
ACTTTTTACCTCTGCCTAATCATCTCTTGTACATGTCCCCTGTTC AAG

4060 4070 4080 4090 4100
CCTCCAAGCTGTGCCTTGGGTGGCTTTGGGGCATGGACATTGACCCTTAT

4110 4120 4130 4140 4150
AAAGAATTTGGAGCTACTGTGGAGTTACTCTCGTTTTTGCCTTCTGACTT

4160 4170 4180 4190 4200
CTTTCCTTCCGTCAGAGATCTCCTAGACACCGCCTCAGCTCTGTATCGAG

4210 4220 4230 4240 4250
AAGCCTTAGAGTCTCCTGAGCATTGCTCACCTCACCATACTGCACTCAGG

4260 4270 4280 4290 4300
CAAGCCATTCTCTGCTGGGGGGAATTGATGACTCTAGCTACCTGGGTGGG

4310 4320 4330 4340 4350
TAATAATTTGGAAGATCCAGCATCCAGGGATCTAGTAGTCAATTATGTTA

4360 4370 4380 4390 4400
ATACTAACATGGGTTTAAAGATCAGGCAACTATTGTGGTTTCATATATCT

4410 4420 4430 4440 4450
TGCCTTACTTTTGGGAAGAGAGACTGTACTTGAATATTTGGTCTCTTTCGG

4460 4470 4480 4490
AGTGTGGATTTCGCACTCCTCCAGCCTATAGACCACCAAATGCCCT

Figure 14F